

## High Throughput Multiplex DNA Sequence Amplifications

### Reference to Government Grant

This invention is made with government support under grant R01-HG02094 awarded  
5 by the National Human Genome Research Institute. The U.S. government may have certain  
rights in this invention.

### Field of the Invention

This invention pertains to the field of high throughput multiplex DNA sequence  
amplification. Specifically, the invention pertains to methods of designing primers that allow  
10 the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase  
chain reaction and minimize the formation of nonspecific extension of undesired DNA  
fragments.

### Background

The polymerase chain reaction (PCR) is a primer-directed *in vitro* reaction for the  
15 enzymatic amplification of a specific DNA fragment. Saiki, Enzymatic Amplification of  $\beta$ -  
Actin Genomic Sequences and Restriction Site Analysis for Diagnosis of Sickle Cell Anemia,  
*Science* 230: 1350-54 (1985). The PCR process is involved in the repetitive cycles of  
denaturation, primer annealing and extension by a thermostable DNA polymerase of two  
oligonucleotide primers that flank the DNA region of interest in a template DNA sample. At  
20 the beginning the PCR process, the duplex DNA target is denatured into two separated  
strands of DNA through a first heating step. In a subsequent annealing step, each  
oligonucleotide primer anneals or hybridizes to the complementary sequence of one separated  
strand of the target DNA. In a third extension step, nascent DNA is synthesized by extending

each primer from its 3' hydroxyl end of towards the 5' end of the annealed target DNA strand by a thermostable DNA polymerase. The heating or denaturation step, the primer annealing step and the enzymatic extension step together constitute a single PCR cycle. If the newly synthesized DNA strand extends to or beyond the region complementary to the other primer, it serves as a primer annealing site and a template for extension in a subsequent PCR cycle. As a result, the repetitive PCR cycles give rise to the exponential accumulation of a specific DNA fragment whose termini are defined by the 5' ends of the two primers. Theoretically, at the  $n$ th cycle of the PCR process, a single DNA molecule can produce  $2^n$  progeny DNA fragments of interest.

The distinctive nature of the PCR process in producing a substantive quantity of DNA fragments of interest from an initial tiny amount of DNA sample has gained broad applications in the field of biomedical research and clinical diagnosis. For example, PCR has been widely used in the diagnosis of inherited disorder and the individualization of evidence samples in the forensics area. Erlich *et al*, Recent Advances in the Polymerase Chain Reaction, *Science* 252: 1643-51 (1991); Newton & Graham, PCR (Oxford, 1994). In particular, PCR has played a critical role in genotyping a vast number of genetic polymorphisms and individual variations which underlie the onset of many diseases. Shi, Enabling Large-Scale Pharmacogenetic Studies by High-throughput Mutation Detection and Genotyping Technologies, *Clin. Chem.* 47: 164-172 (2001).

Widespread applications notwithstanding, the use of PCR is quite often limited by cost, time, and the availability of adequate test samples. To illustrate, the human genome project has placed over 6000 DNA markers in human genetic mapping. To analysis these 6000 markers in 1000 specimens, a total of 6,000,000 PCR reactions are needed if only one

marker sequence is amplified in each reaction. As a well equipped laboratory may process 300 reactions and post-PCR assay a day, it will take a total of 20,000 working days or 80 years to complete the analysis, provided that the amount of each specimen suffices 6000 reactions.

5 In overcoming these limitations, a variant PCR termed multiplex PCR has been developed. Chamberlian *et al*, Deletion Screening of the Duchenne Muscular Dystrophy Locus via Multiplex DNA Amplification, *Nucleic Acids Res.* 16: 11141-56 (1988). Unlike the standard or uniplex PCR where only one pair of primers is used to amplify a single DNA fragment of interest, the multiplex PCR includes more than one pair of primers and thus  
10 results in more than one DNA fragment. Since its inception, the multiplex PCR has been applied in many areas of DNA testing, including gene deletion analysis, Chamberlain, *supra*, mutation and polymorphism analysis, Rithidech *et al*, Combining Multiplex and Touch Down PCR to Screen Murine Microsatellite Polymorphism, *Bio-Techniques* 23: 36-45 (1997), quantitative analysis, Zimmermann *et al*, Quantitative Multiple Competitive PCR of HIV-  
15 DNA in a Single Reaction Tube, *BioTechniques* 21: 480-484 (1996), RNA detection, Zou, Identification of New Influenza B virus Variants by Multiplex Reverse Transcription-PCR and the Heteroduplex Mobility Assay, *J. Clin. Microbiol.* 36: 1544-1548 (1998), and identification of microorganisms, Elnifro *et al*, Multiplex PCR: Optimization and Application in Diagnostic Virology, *Clin. Microbiol. Rev.* 13: 559-570 (2000).

20 Conceptually, the multiplex PCR has the potential to produce considerable savings in cost, time and sample volume. In aforementioned project of analyzing 6000 DNA markers in 1000 specimens, if  $n$  pairs of primers are used in a multiplex PCR reaction, it will only cost one- $n$ th of 20,000 working days to complete the project as well as one- $n$ th of the cost and

sample volume required in the uniplex PCR reactions. Despite the attractive potential, the application of the multiplex PCR poses many challenges. For example, even under carefully optimized reaction conditions, only 26 DNA fragments could be amplified simultaneously in a single multiplex PCR. Edwards & Gibbs, Multiplex PCR: Advantages, Developments and

5 Applications, *PCR Meth. Appl.* 3: S65-75 (1994); Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

Researchers are facing two tiers of challenge in optimizing the multiplex PCR. The first tier of challenge is the efficacy of PCR. In general, this issue is ubiquitous in all PCR  
10 reactions, whether in multiplex PCR or uniplex PCR. The efficacy of PCR is measured by its specificity, efficiency and fidelity. A highly specific PCR will generate one and only one amplified DNA fragment of intended sequence from each pair of primers. More efficient amplification will generate more products with fewer PCR cycles. A high-fidelity PCR product has the minimal amount of DNA polymerase-induced errors. Studies have shown the  
15 efficacy of PCR is affected by factors including the primer annealing temperature, the activity and concentration of the thermostable DNA polymerase, the PCR buffer components such as dNTPs and MgCl<sub>2</sub>, and the first cycle set-up. Roux, Optimization and Troubleshooting in PCR, *PCR methods Appl.* 4: S185-S194 (1995); Roberston & Walsh-Weller, An Introduction to PCR Primer Design and Optimization of Amplification Reactions, *Methods Mol. Biol.* 98:  
20 121-154 (1998). Special attention has also been paid to the primer parameters, such as homology of primers with their target DNA sequence, primer length, GC content, ratio of primers to the template DNA. Researchers are cautioned that the efficacy of PCR is often a delicate balance among specificity, efficiency and fidelity. Cha & Thilly, Specificity,



Efficiency, and fidelity of PCR, *PCR Methods. Appl.* 3: S18-S19 (1993). Adjusting the conditions for specificity may compromise the efficiency or fidelity and *vice versa*.

The second tier of challenge in multiplex PCR is the presence of multiple pairs of primers that are unique to multiplex PCR. It is reported that the presence of more than one primer pair increases the chance of obtaining spurious amplification products, primarily because of the formation of nonspecific DNA extensions, e.g., primer dimers. Markoulatos *et al*, Multiplex Polymerase Chain Reaction: A Practical Approach, *J. Clin. Lab. Anal.* 16: 47-51 (2002). The nonspecific extensions occur when 1) a first primer non-specifically interacts with a second primer because the first primer shares a certain degree of complementarity in its 3' sequence with the 3' sequence of the second primer; and 2) when a primer non-specifically interacts with a DNA sequence of a template DNA which is not the target DNA sequence. Elnifro, *supra*. The nonspecific extensions undermine not only the specificity of PCR but the efficiency as well. The nonspecific products compete with desired target DNA, consume the limited supplies of enzymes, primers and nucleotides, and produce impaired rates of annealing and extension. Markoulatos, *supra*. Not surprisingly, the non-specific extension limits the number of desired DNA fragments in a single multiplex PCR and poses a major limitation to the application and efficacy of multiplex PCR. Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

So far little progress has been made in combating the nonspecific extension problem. Researchers have developed a method to lower the chance of forming the nonspecific extension by adding a universal tail sequence to the 5' end of the sequence-specific primers.

Lin *et al, supra*; Brownie et al, The Elimination of Primer-Dimer Accumulation in PCR,

*Nucleic Acids Res.* 25: 3235-3241 (1997). The tailed primers are added in a multiplex PCR reaction at very low concentrations and allowed to participate the early cycles of reaction. In subsequent cycles, the primers complementary to the universal tail sequence are added into the reaction at high concentrations and proceeded to continue PCR cycles. This method has reportedly produced 26 DNA fragments and minimized the accumulation of non-specific extensions. Lin *et al, supra*. However, the addition of a tail sequence does not thoroughly tackle the problem of non-specific interaction among primers or between a primer and a target DNA.

Thus, there is a need in the art to design primers that allow the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase chain reaction. There is a need in the art to design primers that minimize or substantially reduce the formation of nonspecific extension of undesired DNA fragments. There is a need in the art to design primers that significantly enhance the efficacy of multiplex polymerase chain reactions.

#### Brief Description of the Drawings

Fig. 1 is an illustration of five forms of primer-primer interactions.

Fig. 2 is an illustration of three forms of interactions between primers and nonspecific target templates.

Fig. 3 is an illustration of a genotyping microarray determining the genotypes of a DNA sample at the 627 loci.

Fig. 4 is an illustration of a set of criteria in designing primers that are experimentally acceptable.

### Summary of the Invention

One aspect of the present invention relates to methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

In one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a first primer and a second primer or the first primer comprises the steps of aligning the first primer and the second primer and selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.
- 5) the maximal match between the first primer and the second primer does not exceed 75%.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a

template DNA comprises the steps of aligning the primer and the template DNA and selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and 2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer;
- 5) the first primer at its 3' end does not contain 15 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary;

6) the primer at its 3' end does not contain 18 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

7) the maximal match between the first primer and the second primer used in the multiplex amplification does not exceed 75%.

Another aspect of the present invention relates to computer products or computer programs which, once executed by a computer process, perform methods as disclosed in the present invention.

The methods according to the present invention increase the number of desired DNA fragments, enhance the efficacy of the multiplex PCR and achieve a significant reduction in cost, time and sample volume. A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments.

The methods according to the present invention significantly broaden the application of multiplex PCR in the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, the gene expression profiling in various samples, and high throughput genotyping technologies which include oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

### Detailed Description of the Invention

The primary aspect of the present invention provides methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

The nonspecific extension of unwanted DNA fragments is a major factor in preventing effective applications of multiplex PCR. The nonspecific extension is caused by nonspecific interactions between different molecules of either the same primer, or different primers, or a primer and a non-primer specific region of DNA templates. Specifically, the nonspecific interactions are caused by 1) a stretch of perfectly matched sequence at the 3' ends of two primers, 2) a stretch of perfectly matched sequence with only one mismatch at the 3' ends of two primers, 3) a stretch of the 3' end sequence of a primer perfectly matching to the internal sequence of the same primer, another primer, or a non-primer specific region of a DNA template, 4) a stretch of the 3' end sequence of a primer perfectly matching with only one mismatch to the internal sequence of itself, another primer, or a non-primer specific region of a DNA template, or 5) a stretch of a sequence in a primer matching to itself, another primer, or a non-primer specific region of a DNA template. Fig. 1. The nonspecific extensions of undesired DNA fragments compete and consume the same reagent components in the PCR reaction and thus impair the production and extension of desired DNA fragments. The problem of nonspecific extensions is aggravated when multiple pairs of primers of high concentrations are present in a single multiplex PCR.

One embodiment of the present invention circumvents the nonspecific extension by setting forth a list of criteria in designing PCR primers useful for multiplex PCR. According

to one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and all the rest of primers including the primer comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are  
5 perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are  
10 perfectly matching to a sequence anywhere of the first primer or the second primer; and
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.

The same method repeatedly applies to the selection of a subsequent primer until all  
15 the selected primers meet the above criteria.

According to another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a template DNA comprises the steps of selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly  
20 matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

According to another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

5 5) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;

6) the first primer at its 3' end does not contain seven or more bases that are  
10 perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;

7) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;

8) the first primer at its 3' end does not contain eleven or more bases that are  
15 perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer,

9) the first primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

20 10) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.



In practicing the present invention, each primer to be used in a multiplex PCR is selected through the methods described herein. The selection of primers for a large number of DNA templates can be conducted manually or through a computer system. In a preferred embodiment, the methods according to the present invention are conducted through the use of  
5 a computer system.

A computer system according to the present invention refers to a computer or a computer readable medium designed and configured to perform some or all of the methods as described herein. A computer used herein may be any of a variety of types of general-purpose computers such as a personal computer, network server, workstation, or other computer  
10 platform now or later developed. As commonly known in the art, a computer typically contains some or all the following components, for example, a processor, an operating system, a computer memory, an input device, and an output device. A computer may further contain other components such as a cache memory, a data backup unit, and many other devices. It will be understood by those skilled in the relevant art that there are many possible  
15 configurations of the components of a computer.

A processor used herein may include one or more microprocessor(s), field programmable logic arrays(s), or one or more application specific integrated circuit(s). Illustrative processors include, but are not limited to, Intel Corp.'s Pentium series processors, Sun Microsystems' SPARC processors, Motorola Corp.'s PowerPC processors, MIPS  
20 Technologies Inc.'s MIPS processors, and Xilinx Inc.'s Vertex series of field programmable logic arrays, and other processors that are or will become available.

A operating system used herein comprises machine code that, once executed by a processor, coordinates and executes functions of other components in a computer and

facilitates a processor to execute the functions of various computer programs that may be written in a variety of programming languages. In addition to managing data flow among other components in a computer, an operating system also provides scheduling, input-output control, file and data management, memory management, and communication control and related services, all in accordance with known techniques. Exemplary operating systems include, for example, a Windows operating system from the Microsoft Corporation, a Unix or Linux-type operating system available from many vendors, any other known or future operating systems, and some combination thereof.

A computer memory used herein may be any of a variety of known or future memory storage devices. Examples include any commonly available random access memory (RAM), magnetic medium such as a resident hard disk or tape, an optical medium such as a read and write compact disc, or other memory storage devices. A memory storage device may be any of a variety of known or future devices, including a compact disk drive, a tape drive, a removable hard disk drive, or a diskette drive. Such types of memory storage device typically read from, and/or write to, a computer program storage medium such as, respectively, a compact disk, magnetic tape, removable hard disk, or floppy diskette. Any of these computer program storage media, or others now in use or that may later be developed, may be considered a computer program product. As will be appreciated, these computer program products typically store a computer software program and/or data. Computer software programs, also called computer control logic, typically are stored in system memory and/or the program storage device used in conjunction with memory storage device.

In one embodiment, a computer program product as described herein comprising a computer memory having a computer software program stored therein, wherein the computer

software program when executed by a processor or in a computer performs methods according to the present invention.

An input device used herein may include any of a variety of known devices for accepting and processing information from a user, whether a human or a machine, whether local or remote. Such input devices include, for example, modem cards, network interface cards, sound cards, keyboards, or other types of controllers for any of a variety of known input function. An output device may include controllers for any of a variety of known devices for presenting information to a user, whether a human or a machine, whether local or remote. Such output devices include, for example, modem cards, network interface cards, sound cards, display devices (for example, monitors or printers), or other types of controllers for any of a variety of known output function. If a display device provides visual information, this information typically may be logically and/or physically organized as an array of picture elements, sometimes referred to as pixels.

As will be evident to those skilled in the relevant art, a computer software program of the present invention can be executed by being loaded into a system memory and/or a memory storage device through one of the above input devices. On the other hand, all or portions of the software program may also reside in a read-only memory or similar type of memory storage device, such devices not requiring that the software program first be loaded through input devices. It will be understood by those skilled in the relevant art that the software program or portions of it may be loaded by a processor in a known manner into a system memory or a cache memory or both, as advantageous for execution.

As will be appreciated by those skilled in the art, a computer program product of the present invention, or a computer software program of the present invention, may be stored on

and/or executed in a PCR instrument. For example, a computer software of the present invention can be installed in, for example, the Smart Cycler System, the Idaho Rapid Cycler, the Carbett Roter-Gene System, the GeneAmp 5700 Sequence Detection System, the ABI Prism7000, 7700 & 7900 Sequence Detection Systems, the iCycler System, the MX-4000  
5 Multiplex Quantitative PCR System, the DNA Engine Opticon System, the Perkin-Elmer 9600 cycler, and MJ Research's DNA Engine Opticon System.

However, it is not necessary that the computer program product or the computer software program be stored on and/or executed in a PCR instrument. Rather, the computer product or software may be stored in a separate computer or a computer server which may or  
10 may not connect to the PCR instrument through a data cable, a wireless connection, or a network system. As commonly known in the art, network systems comprise hardware and software to electronically communicate among computers or devices. Examples of network systems may include arrangement over any media including Internet, Ethernet 10/1000, IEEE 802.11x, IEEE 1394, xDSL, Bluetooth, 3G, or any other ANSI approved standard.

15 In a preferred embodiment, a computer program termed MULTIPLEX is developed to select primers according to the methods as described in the present invention. See Table I for the flowchart of MULTIPLEX program.

Even with the assistance of MULTIPLEX, it is time consuming to analyze exhaustively all possible sequences frames and select the best possible frames for PCR  
20 primers. To expedite the computer-assisted selection process, a strategy termed "random fitting" is developed. Under the random fitting strategy, a set of criteria for the length of the matching sequences is set forth for primer selection. See Table I.. For example, when the number of 3' end matching bases is less than 4, the experimental effect of this

complementarity is neglected. Therefore, the criterion for the length of 3' end complementarity was set to be less than four. With the predefined criteria, the MULTIPLEX computer program first randomly picks up a pair of primers for each target sequence. All possible interacting pairs in this combination are examined. Record is made on qualified and unqualified primers in the combination. The program then randomly picks up a new pair of primers for each target sequence that collectively form a second combination. If the number of qualified primers in the second combination is less than that in the first combination, no record is made. The MULTIPLEX program, however, begins to examine a third combination. If the number of qualified primers in the third combination is greater than that in the first combination, the first primer combination is replaced by the third one in record. The program keeps processing until a combination with all qualified primers is found. Under the random fitting strategy, the MULTIPLEX program can select qualified primers for 100 sequences within two hours, 500 within two days and 1,000 within two weeks. The "qualified primers" are those primers fully conforming with the selection criteria set forth in the method of the present invention.

To further improve the MULTIPLEX program, another primer selection method called linear primer selection is also used as an alternative. See Table I. With this strategy, instead of selecting the frames randomly, each frame of a pair is selected from one end of the defined range of a sequence. The selected frame pair is then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding sequence is completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences. The newly selected frames are then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding

sequence is then completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences... If the frames are slid to the other ends but not qualified frames are found, the lengths of the frames will be increased by 1 base. The same process described above will be repeated. The sliding and length changing process repeats until a pair of qualified frames is found. If no qualified frames can be found after exhausting all possible frames for a sequence, the sequence will be labeled as unusable, and will be excluded from the multiplex set. This method is called linear primer selection.

When the number of sequences is large, the random primer selection method may be used for selecting primers of only a fraction of sequences. The random selection process is stopped at a point defined by the user. The program can then switch to linear primer selection method. We have shown that appropriate combination of these two methods can increase the selection speed by several tens to >100 fold compared with using the random method only.

It needs to be pointed out that the MULTIPLEX method can be used not only for primer selection of SNPs, but also for primer selection of any other DNA and RNA sequences if a position is defined so that it can be used to separate a sequence into two parts for selecting the two primers, respectively.

Following the selecting and synthesizing of qualified primers, DNA templates are contacted with multiple primers for the amplification of desired DNA fragments under conditions suitable for multiplex PCR developed in the inventor's laboratory. These conditions are: 2.0 mM MgCl<sub>2</sub>, 50 mM KCl, 100 mM Tris-HCl, pH 8.3, 100 μM deoxynucleotide triphosphates (dNTPs), and 10 units/50 μl "HotStart" *Taq* DNA polymerase (Qiagen, Valencia CA). The PCR mix is first preheated for 15 min at 94°C to activate the DNA polymerase followed by 40 PCR cycles. Each cycle consists of a denaturation step at

94°C for 40 sec, and then an annealing step at 55°C for 2 min followed by a ramping step from 55°C to 70°C within 5 min. After the PCR cycles, the samples are incubated at 72°C for 3 min.

A DNA template to be used in practicing the present invention includes without  
5 limitation eukaryotic, prokaryotic and viral DNA. The DNA may be obtained from any cell source or body fluid. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Body fluids include blood, urine, cerebrospinal fluid, semen and tissue exudates at the site of infection or inflammation. DNA  
10 is extracted from the cell source or body fluid using any of the numerous methods that is standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source. The preferred amount of DNA to be extracted for use in the present invention is at least 5 pg which is corresponding to about 1 human cell equivalent of a genome size of  $4 \times 10^9$  base pairs.

15 A primer designed in accordance to the method in the present invention is from 17 to 50 nucleotides in length, preferably 20 to 35 nucleotides in length. The concentration of a primer in the multiplex PCR reaction can range from 0.1nM to about 4μM per reaction, preferably from 1nM to 0.1 4μM per reaction.

Multiplex PCR reactions are carried out using manual or automatic thermal cycling.  
20 Any commercially available thermal cycler may be used, such as, e.g., a Perkin-Elmer 9600 cycler.

The resultant multiple amplified DNA fragments of interest are analyzed using any of several methods that are well-known in the art. For example, agarose or polyacrylamide gel

electrophoresis is used to rapidly resolve and identify each of the amplified sequences. When a gel is used, different amplified sequences are preferably of distinct sizes and thus can be resolved in a single gel. The reaction mixture can further be treated with one or more restriction endonucleases prior to electrophoresis. Alternative methods of product analysis include without limitation dot-blot hybridization with allele-specific oligonucleotides, single-strand conformational polymorphism analysis, high-throughput genotyping platforms including oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

The multiple primers designed in accordance to the method in the present invention minimize the nonspecific interaction between primers or between a primer and nonspecific target sequence of a template DNA. Accordingly, the use of these primers in a multiplex PCR minimizes the formation of non-specific extension of undesired DNA fragments and maximizes the specific interaction and amplification of desired DNA fragments.

Furthermore, the method in the present invention increases the number of desired DNA fragments, enhances the efficacy of the multiplex PCR and achieves a significant reduction in cost, time and sample volume. Finally, the multiple primers designed in accordance with the methods of the present invention may be used in real time PCR or multiplex real time PCR.

A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments. It is preferred that the single multiplex PCR contain at least 100 pairs of primers and produce at least 100 desired DNA fragments.



The present invention significantly broadens the application of multiplex PCR in the art which has been limited by the nonspecific extensions of unwanted DNA fragment and the number of desired DNA fragments it could produce. Given a large number of multiple desired DNA fragments that a multiplex PCR now can produce using primers designed under the present invention, the multiplex PCR can now be fully used in applications including but not limited to the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations in cancers, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, and the gene expression profiling in various samples.

The following examples are intended to further illustrate the present invention without limiting the invention thereof.

EXAMPLE 1. Selection of 627 pairs of primers.

648 single nucleotide polymorphism (SNP) markers were initially selected from the SNP Database maintained by the National Center for Biotechnology Information. To facilitate the genotyping after PCR, all these SNPs were transition polymorphisms that were A to G or C to T changes at their polymorphic sites. All SNP sequences were analyzed by the computer program MULTIPLEX to determine whether these SNP sequences are unique in the genome. The repetitive sequences were discarded. PCR primers were selected by using the computer program MULTIPLEX described above with the following values:  $T_m$  range = 75-104°C, primer length range = 24-33 bases, 3' perfect matches <4, 3' match with 1 mismatch <7, 3' end matching internal sequences of other molecules <9; 3' end matches internal sequences of other molecules with 1 mismatch <11; maximal match between different molecules, 75%). The quality of each pair of primers was examined individually by using them to amplify their

target sequences. Only the primer pairs with high specificity and yield, as judged by gel electrophoresis, were used for multiplex amplification. At the end, a panel of 627 SNPs was selected from the initial 648 SNPs as shown in Table II and Table III. Table II is an illustration of a list of 627 single nucleotide polymorphism (SNP) markers selected from 648 SNP markers. Table 3 is an illustration of a list of 627 pairs of primers and probes that were designed according to the method disclosed in the embodiment of the invention, used in a single multiplex PCR reaction, and used for genotype determination by analyzing the multiplex PCR products by microarray.

EXAMPLE 2. Using 622 pairs of selected primers in a single multiplex PCR.

For the multiplex PCR, lysate for 500 cells from a tissue cultured cell line, MG2314, was prepared. The reason for using cells instead of purified DNA is that they could be precisely quantified and equal number of nearly equal number of copies of the target sequences could be used as the starting material. PCR mix contained 1 X PCR buffer (100 mM Tris-HCl pH 8.3, 150 mM KCl, 1.5 mM MgCl<sub>2</sub>, and Gelatin 100 µg/ml), primers (10 nM each) for all SNPs, the four dNTPs (100 µM each), Taq DNA polymerase (5 units) with a final volume of 30 µl. Sample was preheated for 15 min at 95°C. Each PCR cycle consisted of a denaturation step at 95°C for 40 sec; annealing at 55°C for 3 min; and a step for both annealing and extension with temperature ramping from 55°C to 70°C within 5 min. A 3 min incubation at 95 °C as added after the PCR cycle to minimize the incompletely extended PCR products. PCR was completed after 40 cycles.

EXAMPLE 3. Analysis of multiple DNA fragments after the multiplex PCR

To resolve the allelic products in the multiplex PCR product for genotype determination, single base extension and microarray methods were used. Two

oligonucleotides with completely complementary sequences for each SNP were synthesized for this purpose. One of these was called E probe that was using in the single base extension assay. The other was called A probe that was spotted onto a coated glass slide. E probes had sequences with their 3'-ends next to their polymorphic sites. In the single base extension  
5 assay, dideoxynucleotides labeled with either the chromophore Cy 3 or Cy 5 were used. The allelic base at the polymorphic site determined which fluorescently labeled nucleotide could be incorporated into an E probe.

The corresponding A probes were spotted onto a glass slide with a microarrayer manufactured by Cartesian. The fluorescently labeled E probes were hybridized with the A  
10 probes on the microarray. The signal intensity for the alleles of each SNP was determined by using the computer software for image analysis from Biodiscovery. See, Fig. 3.

To validate the results from microarray analysis, the genotypes of the cell line used in the study were determined for all 622 SNPs by restriction enzyme digestion method described by Li & Hood, Multiplex Genotype Determination at A DNA Sequence Polymorphism  
15 Cluster in The Human Immunoglobulin Heavy-Chain Region, *Genomics* 26: 199-206 (1995). A few SNPs that could not be analyzed by this method were analyzed by direct sequence analysis.

Because all SNP were transition polymorphisms, all E probes could be analyzed by either A and G or T and C. In either case, consistent results from 85% (for labeling with A  
20 and G) to 90% (for labeling with T and C) SNPs were obtained by both microarray and the restriction digestion methods. A probes for A and G labeling were used for 85% of SNPs, and others were replaced by those for T and C labeling. Fig. 5.

Papers and patents listed in the disclosure are expressly incorporated by reference in their entirety. It is to be understood that the description, specific examples, and figures, while indicating preferred embodiments, are given by way of illustration and exemplification and are not intended to limit the scope of the present invention. Various changes and

5 modifications within the present invention will become apparent to the skilled artisan from the disclosure contained herein. Therefore, the spirit and scope of the appended claims should not be limited to the description of the preferred versions contained herein.

## Flow Chart - General

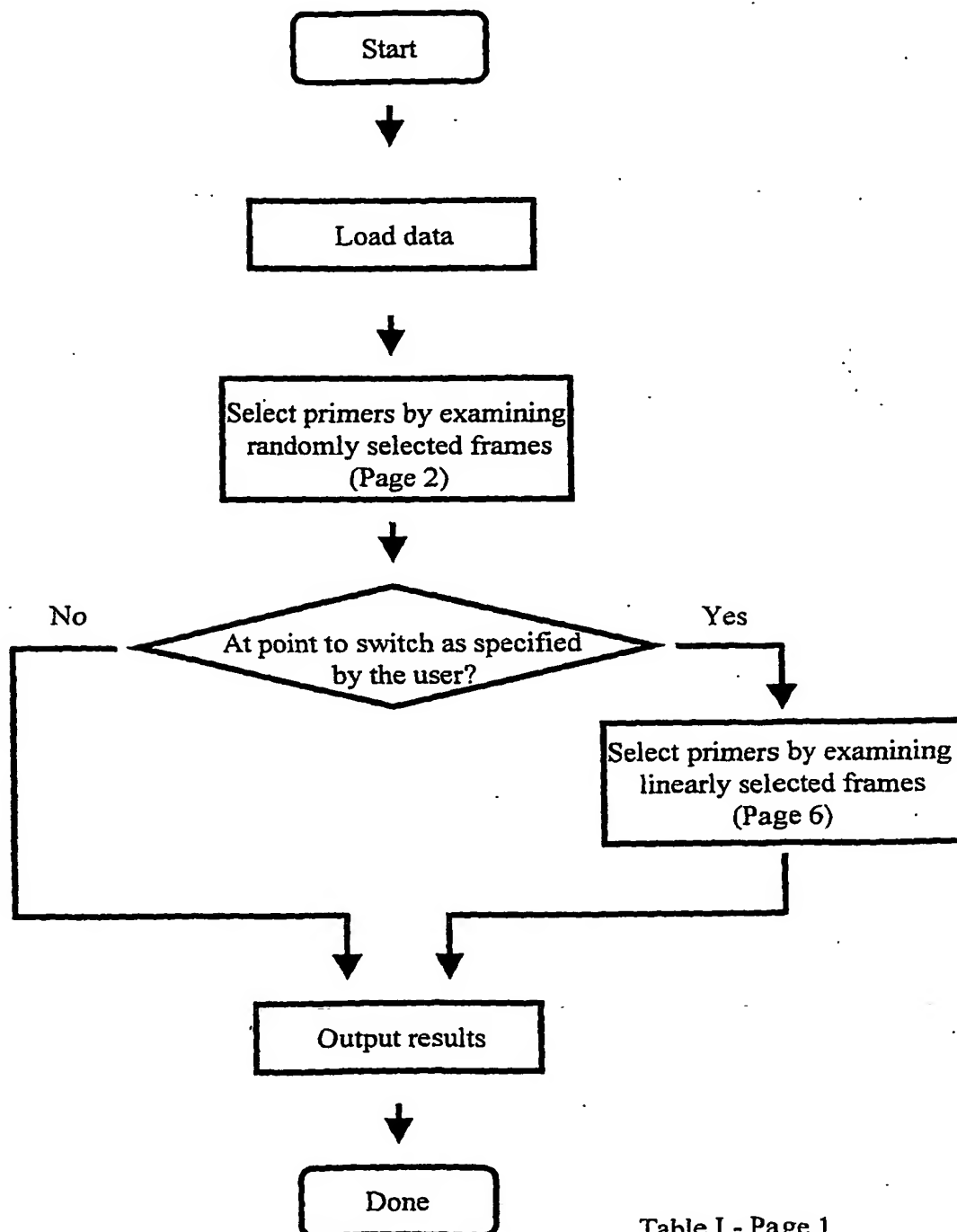


Table I - Page 1

## Page 2 – Select Primers by Examining Randomly Selected Frames

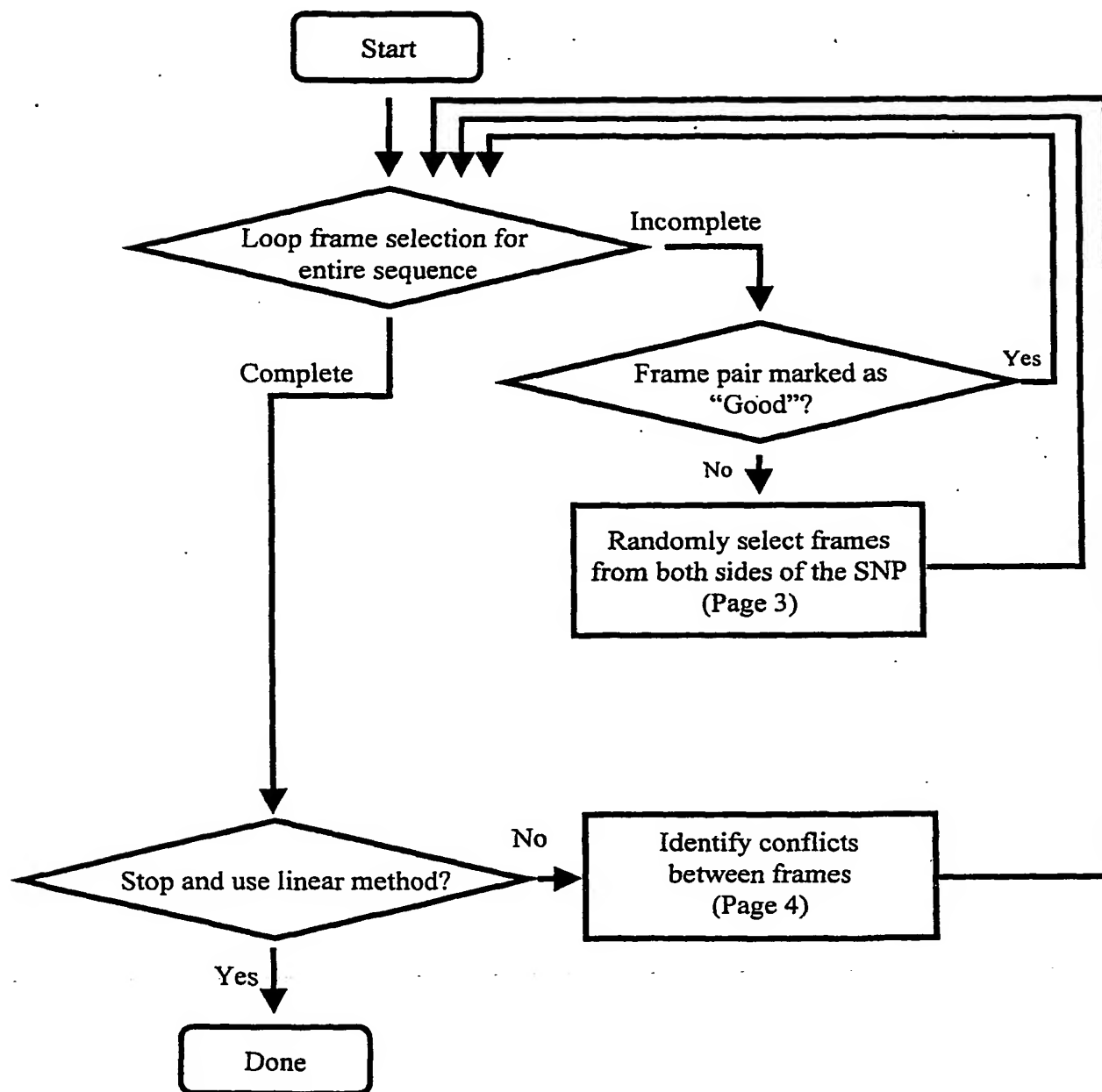


Table I - Page 2

### Page 3 - Randomly Select Frames from Both Sides of Each SNP

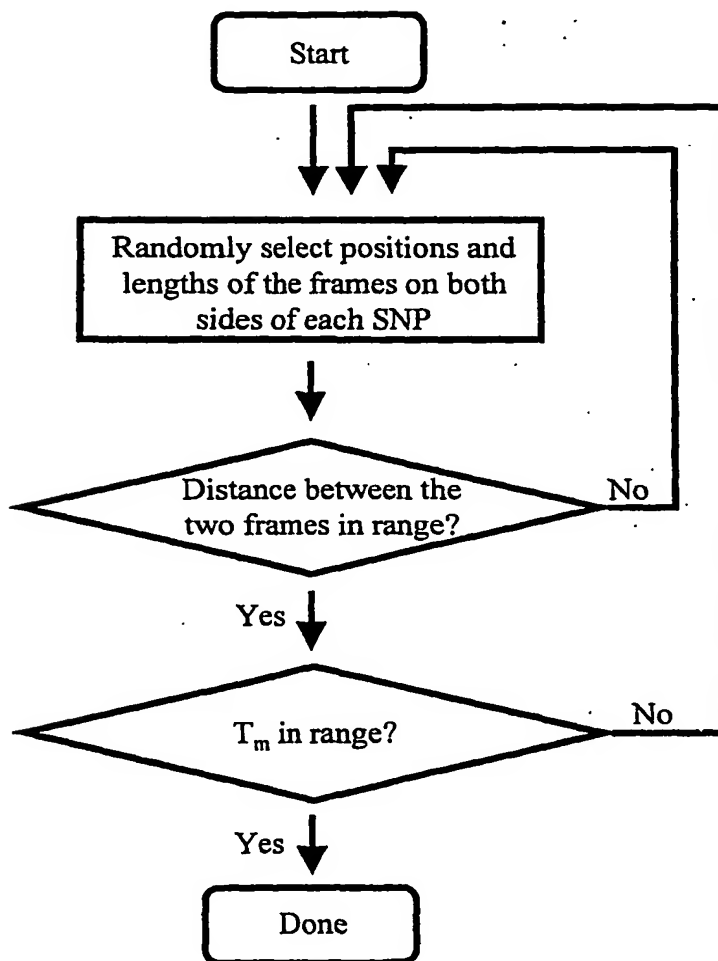


Table I - Page 3

# Page 4 - Identify Conflicts between Frames

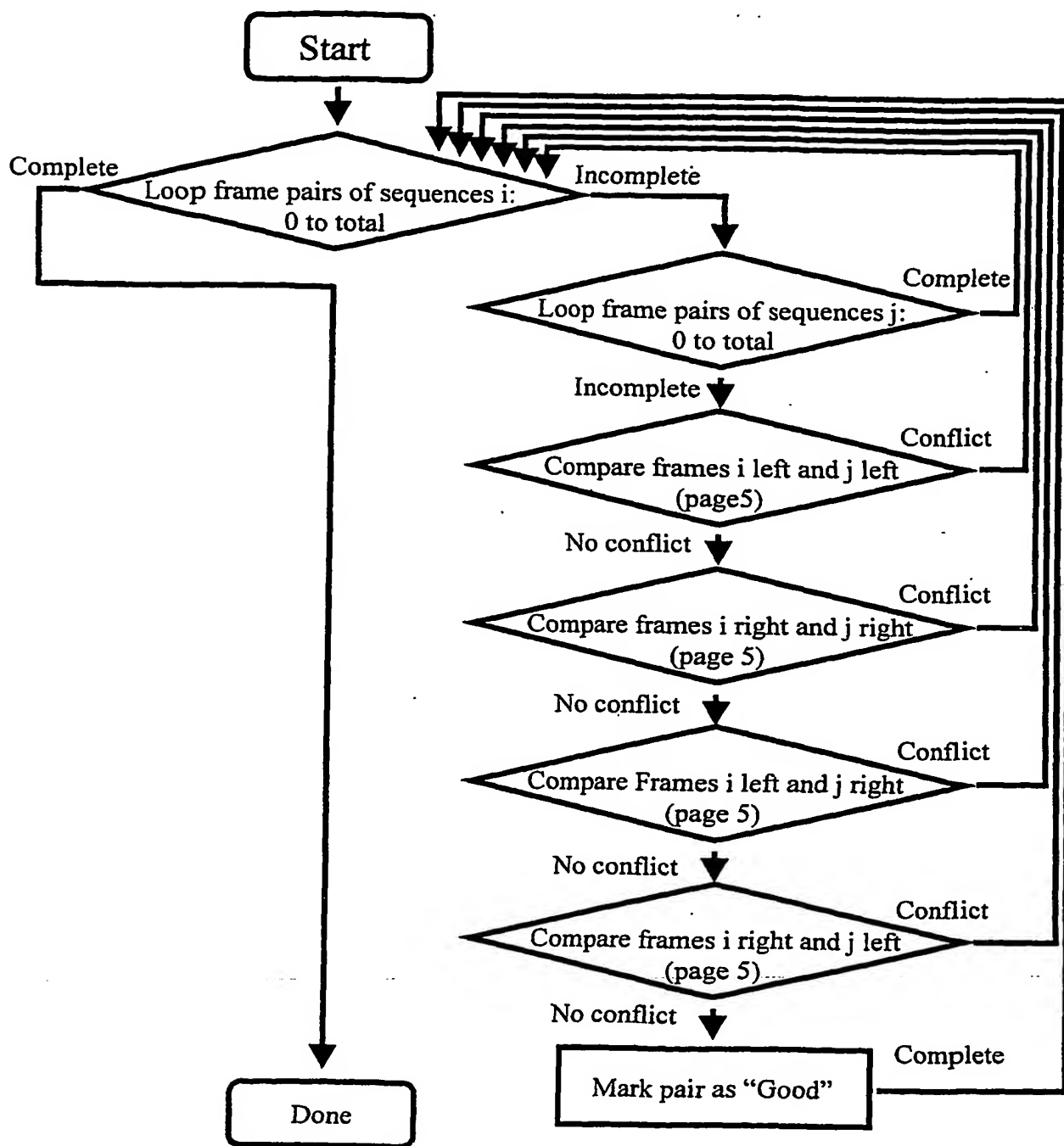


Table I - Page 4



## Page 5 – Compare Selected Frames

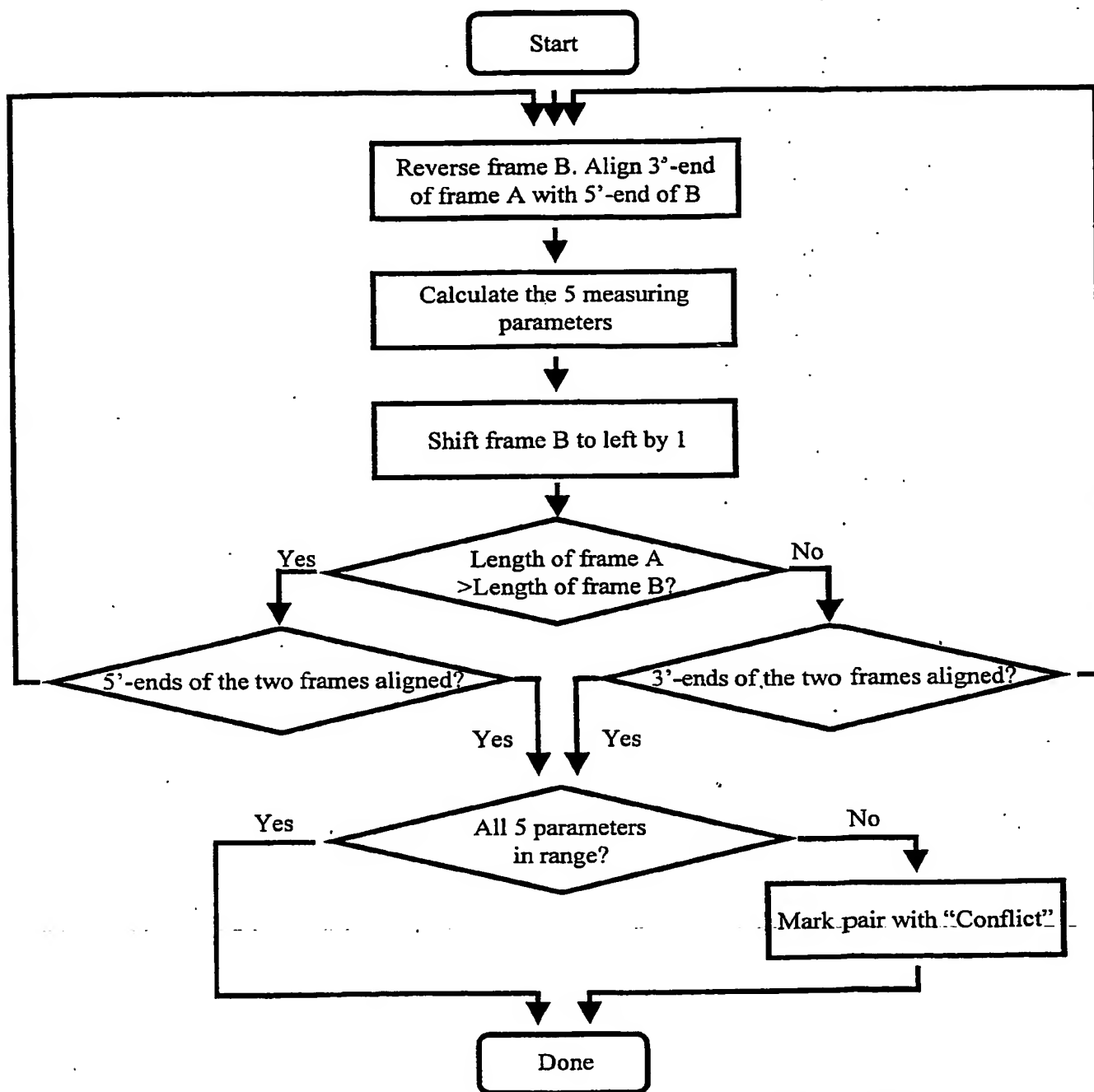


Table I - Page 5

## Page 6 - Select Primers by Examining Linearly Selected Frames

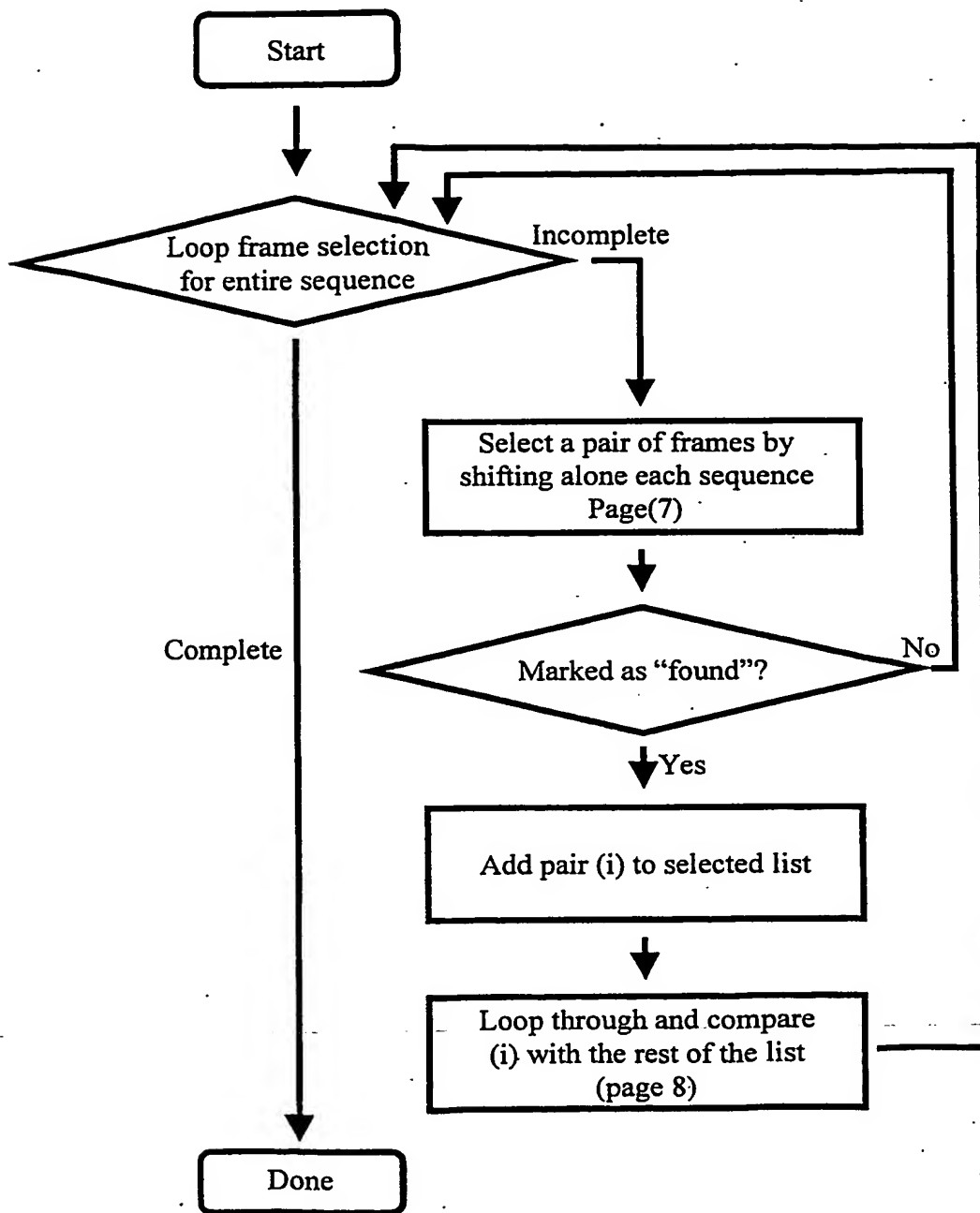
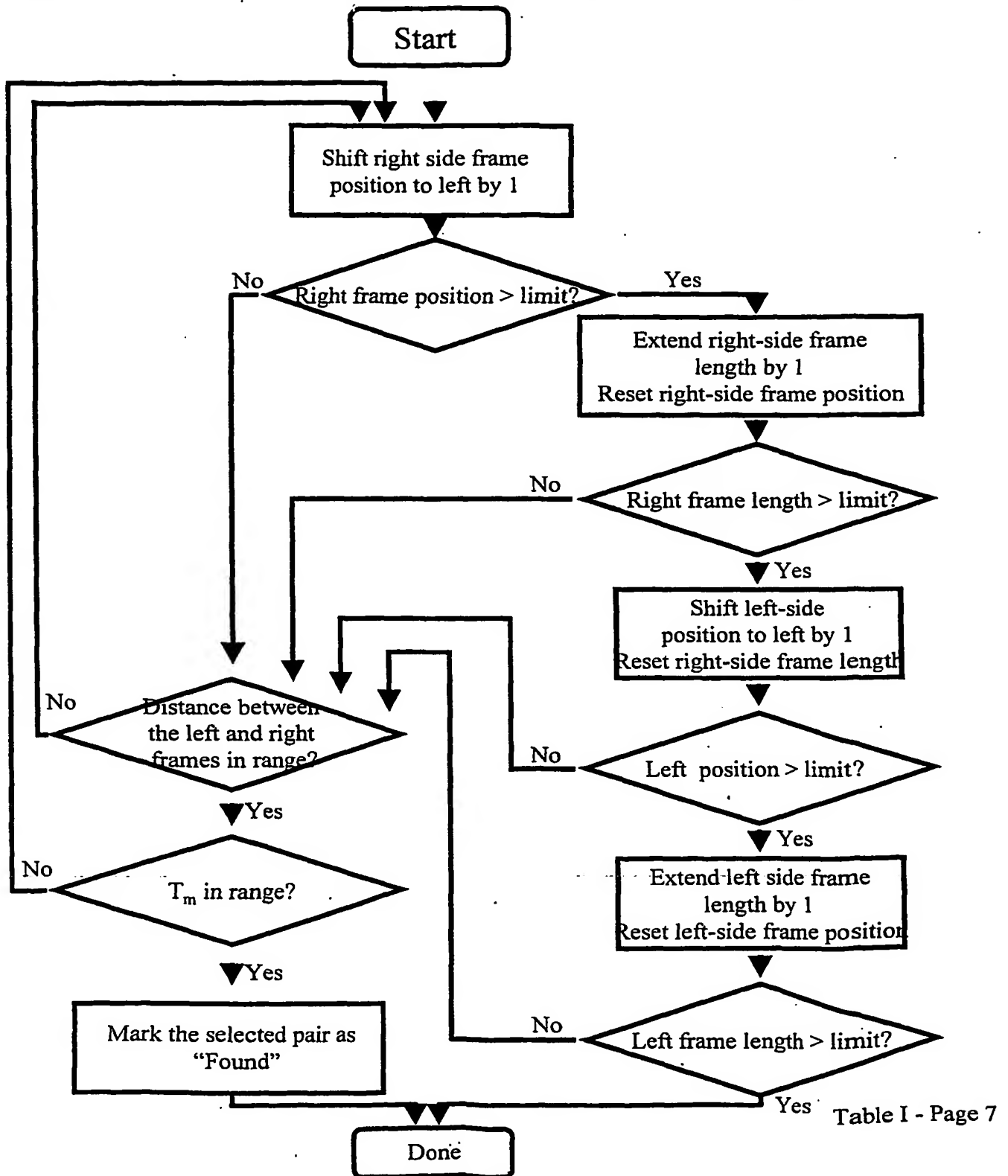


Table I - Page 6

# Page 7 – Select a pair of frames by shifting alone each sequence



## Page 8 - Loop through and Compare Frames i with the Rest of the List

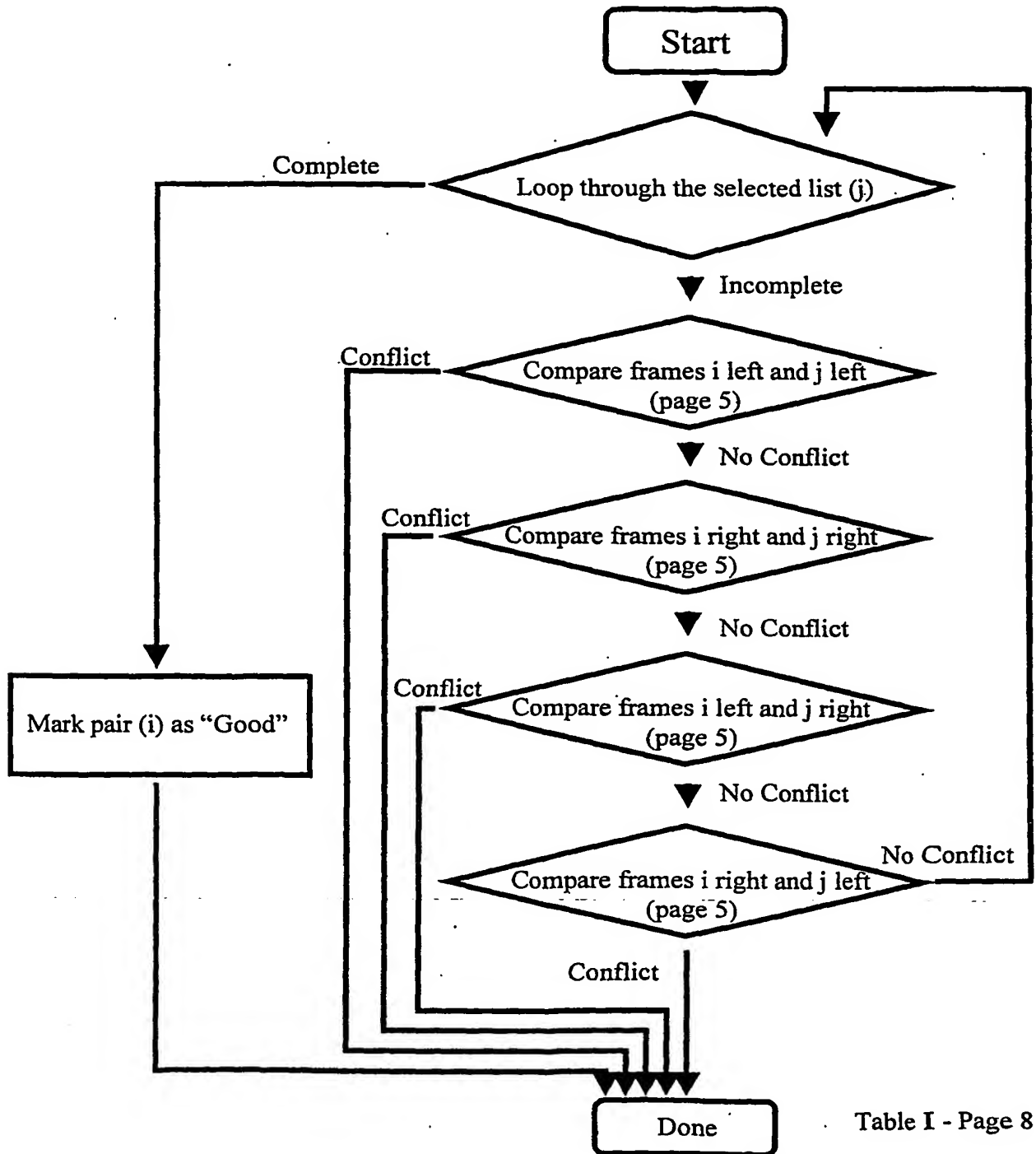


Table I - Page 8

Table 2 Oligonucleotides Used as PCR Primers and as Probes for Genotyping

SNP	Name	Left Primer		Right Primer		Labeled Probe		Probe on Slide	
		Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name
01T002L	01T002L	CACGTGTGAGGCTTTGGTCC	01T002R	GCTCTACCTCTGGACACTCGGGGG	01T002E	GCTCCCACTGCTTCCCGGCAATC	01T002A	OACTGCGGGAGAGCTGGGAGC	01T002A
01T003L	01T003L	CTATAGCCCTCTGAATGGTC	01T003R	TCTGCTCTCCCAAGAGACAC	01T003E	GCTGAAAGCAATAATAGTGTACAGAC	01T003A	GTCGTGACACCAATATGCTTTGACG	01T003A
01T006L	01T006L	AAAGAAGAGAGGTTTGGGGAT	01T006R	CACATGCTGACAGCCGAGAGACTC	01T006E	CTTTCATTAAGAGCTAGAAATTTAGATTC	01T006A	GCAATCTAAATTTCTAGCTGTAAATAAG	01T006A
01T008L	01T008L	ACTAAGGAGGATCAACAACCTC	01T008R	AAGCACTCTTCTTACGTCC	01T008E	CTCTGTGGGGGTGTGTGACACC	01T008A	GGCTGACACGAGCCCAACCAATC	01T008A
01T009L	01T009L	GTACGGTGTCTACAGCAACCA	01T009R	GGGAGCAGCTGTGAGTGGGGCG	01T009E	GATGATTTCTCCGACCTTATCTAATCTC	01T009A	TTTAGCCCAACGAGCCCAAGCCAG	01T009A
01T012L	01T012L	CAACTGAGAGTGTAGTATTTGGA	01T012R	TAGCATCCCAAGCTCTCTTGA	01T012E	GAGTAAATTTCTCCGACCTTATCTAATCTC	01T012A	GAGATTAATAAGTGTGAGCAAAATTAATC	01T012A
01T013L	01T013L	GAATTTCTATCTCACACCGCTGA	01T013R	AGGCTGCTCTGCTCTCACAC	01T013E	GCTTATACAGCAAGGGGTATAAAGGT	01T013A	ACCTTTTATACCCCTGCTGTATTAAGC	01T013A
01T014L	01T014L	ACAGCTGTCCACAGAGTCC	01T014R	TCTCTCTCTGGTCCCTAATG	01T014E	GGCAGAGATTAAGTGTCCAGGACTGTGAA	01T014A	TTCAACAAGTCTCTGACACTTCTCTGCCC	01T014A
01T019L	01T019L	GTGCGCCCACTCTGAGAGAGCTA	01T019R	GTCTCTCTCTGGAGCTCC	01T019E	GGCCCATATTTCTATTCACCTTTGCT	01T019A	AGCAAAAGTGTGAAATAGAAATATGGGC	01T019A
01T020L	01T020L	AACACTTGTCTGGCATATAGTAG	01T020R	GAATGGATGAGACACTCAAT	01T020E	GCTTAAGAAGCAACAGACACTCTCTG	01T020A	CAGGAATGTCTGGGCTCTCTTAGGC	01T020A
01T023L	01T023L	AGATTTCTTGACCTCTCTCTTA	01T023R	AAAGAGATGATTTCAAGGTGAC	01T023E	TTTGCCAGTGTCAATCAAGAGGAC	01T023A	GTCTCTCTGATGACACTTGGCCAAA	01T023A
01T025L	01T025L	AAGGCAATAAGCTGACACTTGA	01T025R	GTACATCTGCTGTCTCAACGCG	01T025E	GGAATTTCAAGGTGTGAGGCGAGAAAG	01T025A	CTTCTCTGGCTCTCTCTGAAATCC	01T025A
01T028L	01T028L	CCAGCGGAGAGCTGTGAAATAG	01T028R	GAAGCAGATCGGGGTGTCTCTCC	01T028E	AGGGCAAGGGCAGAGGGGAGGGTT	01T028A	AACCTCTCTCTGCTGCTCTGCTCT	01T028A
01T029L	01T029L	AAATTAGGCTTTATGTAAATTCAG	01T029R	GAGGCAATAGGCTTTAAATTC	01T029E	GGGTCAAGAGCTGTGCTGACCTTGA	01T029A	TAAGTGGCAAGTCAAGGTCTTGAACCC	01T029A
01T032L	01T032L	CAAAAGACCTCCAAGTCTTAAAAA	01T032R	TCATACCACCAAGGCAAAAA	01T032E	GTTAAGAGATCTCTGCCAATACCT	01T032A	AGGTATTCGGCAAGATCTCTTAAC	01T032A
01T035L	01T035L	GTGCTCATGAGCCGACAGGGG	01T035R	AGGCTGTGAGACAGGGGAC	01T035E	GCTGAGCAGGCCCCCGGTGGCG	01T035A	CGGCCACCGGGGGGCTGCTCAGC	01T035A
01T037L	01T037L	CCATCAGGTAACTGACAAACTCTAA	01T037R	CCCTGAGCCCTGATGCTGGC	01T037E	CTGGCCCTGTACTAGGTCTGTGAAAG	01T037A	CTTCCAGAACTGTAGTACAGGGCCAG	01T037A
01T038L	01T038L	TCTAGCAGGGGGAACAGCC	01T038R	TCAAGGCTCTCTTAAGCGACTC	01T038E	CACCATGCTCTACACAACTTACCC	01T038A	GGGTAGGCTTGTATGACGCAATGGTG	01T038A
01T039L	01T039L	CTCTCTAGTAAACCCGACCT	01T039R	GGCTCTCAGAGCTCTCAAT	01T039E	GAGTCAATCATTAACATAGGGCAT	01T039A	ATGCCCTATTATTATGATGATGATCTC	01T039A
01T041L	01T041L	TCTCAGGTAGTCTGGGGCTGG	01T041R	GGGAAAGTCAAGACTGAGGAGGTG	01T041E	GGCCCTGCTGTCTCCACAGAGGC	01T041A	AGCCAGGCTTGAAGAACAGGGGCC	01T041A
01T042L	01T042L	CTCACTCCCTAGGCTCCGC	01T042R	AGGGAATGATGACGGAACA	01T042E	CCAGTGTCTCTCCACAGAGGC	01T042A	GCCTCTGGGAAAGAGCACTGGG	01T042A
01T043L	01T043L	ATTCTGGAATTTTACGACAC	01T043R	ATTCAGAGGCTTGGCCAGACCTA	01T043E	CACCCAGAGGCTTGTGAAACAGACA	01T043A	TCTGTCTTTCACAGCCCTCTGGGTG	01T043A
01T046L	01T046L	TCTGAACACCCGGTTTATAG	01T046R	GGTCACTGTTTACTCTCAT	01T046E	TCTTAAGAGATATTCCTCATTTTCAAAA	01T046A	TTTGTATTAACATGGGATTAATATCTCTC	01T046A
01T047L	01T047L	CAGAGGGTGTCCGTGCTCTTAA	01T047R	AGGCACTCCACATCTTATGTA	01T047E	TCTTAAGAGATATTCCTCATTTTCAAAA	01T047A	CAGTGAATATACTACCACTGCTATAGA	01T047A
01T048L	01T048L	CACACCTCTAGAGGCTGA	01T048R	AGGCACTCCACATCTTATGTA	01T048E	TCTTAAGAGATATTCCTCATTTTCAAAA	01T048A	TCATCTCTGCTCTTACATGGCTCA	01T048A
01T051L	01T051L	CTACCTGCTCTGGGCTTG	01T051R	CTCATCTCTTCTTCTTACAGAT	01T051E	TGAGTGTGGGGGGGTGTGGG	01T051A	CCCAACACCCCGCCCAACATCA	01T051A
01T054L	01T054L	TGAGATGGCCGACAGCTCCGTG	01T054R	GGCTGTGTTTACTTCCAAAT	01T054E	GCAGTCTGTGCTGCTTCCACAGAGA	01T054A	TCTCTGCTCAAGGTGTGACAGAGCTGC	01T054A
01T055L	01T055L	CTGCGGCGGGTGCAGAGAACT	01T055R	TATGTGAGAGATCTCAGCTC	01T055E	CGAGATGGCTCTCTCCACAGAGA	01T055A	CTCTGTGGGAGGGGCTCTCTG	01T055A
01T056L	01T056L	CACATGGGAAACAATAATCCAAC	01T056R	GGTAGTGTGGGAAATGGTGGAT	01T056E	CTCTCTGAAAAGAGATAGATTTACA	01T056A	TGTAAAGATCTATCTCTTTTTCAGGAAG	01T056A
01T057L	01T057L	CCCATAGCCCATTAACACAGCTTG	01T057R	AAAAACCCACAAAGATATGGCTA	01T057E	CTGCTGCGGAAAGCATGACAGATTACA	01T057A	TGGAGCTGTCAAGCTTACACACATGG	01T057A
01T058L	01T058L	GTGTTCCGGTCCGCAATATGATG	01T058R	CCACACATAAAGAGATATCTAA	01T058E	CGAGATTTATGTCTGGAATAAAGAGATCC	01T058A	GGATCTCTTATTCAGACATAATCTTCC	01T058A
01T060L	01T060L	GAAGTCTACTACACATGAGAGGTA	01T060R	TGCTGGAATGAGTGTGTTCTGCT	01T060E	GGAAGATTTATGTCTGGAATAAAGAGATCC	01T060A	GGCAGAGGCTAGGCTGAGAGATTC	01T060A
01T061L	01T061L	CCAGGCTTCTGCAAGGGGCTGGGTA	01T061R	GGATAGACTATCCCTGCTGGTC	01T061E	CAATGTGTGTGAGCTGTGACAGATTACA	01T061A	TGAGTGAATATTTTGTGAGATGAAAT	01T061A
01T062L	01T062L	AAATGGTACATGCTCTTGTAG	01T062R	ACTAAACCTCTCGGAAATGACA	01T062E	ATTCCTCTACACCAACCTCTACCA	01T062A	TGAGTGAATATTTTGTGAGATGAAAT	01T062A
01T064L	01T064L	GTGGTCTACACAAAGAAACG	01T064R	TTATGCACTATACCTTTGTGAT	01T064E	AAATTAATTTTCAAAAGATATTTGACGTA	01T064A	CAGATACGCTCTGCTCTTCTGCTAG	01T064A
01T065L	01T065L	GGCACTCTGATGATGATCTTA	01T065R	GACAGATTTTCTGTGCTCTTAA	01T065E	CTAGCAAGCCTAGGCTGATCTG	01T065A	AGGGGTAAACAGGGGCTTACTACT	01T065A
01T066L	01T066L	TTGAAAGTCTGCTGTGATAGCCCA	01T066R	CTCCAGTCTGCAACAGCCCTCC	01T066E	GAAGATTAATACCAACCAACCTCTTTTA	01T066A	TAAGAAAGAGGTTGTTGTTGTTATCTTTC	01T066A
01T067L	01T067L	AGAGGATACTTGTAACTGAAA	01T067R	TGTGTGAGTCACTATTTTGTCTA	01T067E	TCCTTAAATGCTAAGCAGCTATAC	01T067A	TAAGAAAGAGGTTGTTGTTGTTATCTTTC	01T067A
01T069L	01T069L	TATCCCTCTGCTCCCTCCGGA	01T069R	CTTTCGCGCTACATTTTCTTCC	01T069E	CTTTAAGCAGAGTGTGCTCCCACTTT	01T069A	TAAGAAAGAGGTTGTTGTTGTTATCTTTC	01T069A
01T070L	01T070L	TGCTCTCTCAGGTAGTATG	01T070R	CTTTCGCGCTACATTTTCTTCC	01T070E	TCCTTGAAGCTTGTGAGCACTTC	01T070A	TAAGAAAGAGGTTGTTGTTGTTATCTTTC	01T070A
01T071L	01T071L	GGCCCTATTTTCAAGAACCAACG	01T071R	AAAGAAATTTGGCTGGCA	01T071E	GGATCTTTGAAATTTGAAATTTCTG	01T071A	GAAGTGCCTCAAGCTTCCCAAGGA	01T071A
01T072L	01T072L	TGTTGCTGATGATCATCTCTT	01T072R	TCTTCAATTTTCAAGAAATTCGG	01T072E	TTCTCTGTGGTATTTATGTTTATATA	01T072A	CCAGAAATTCAGAAATTCAGAAATCC	01T072A
01T074L	01T074L	ATAGCAGCTGAGCTCTCTCTTG	01T074R	GATTTGGGCTGATTTATAGT	01T074E	AAAGTCTCTCTCTCTCTCTGTTT	01T074A	TGTTATTAACACATTAATACCAAGAGAA	01T074A
01T077L	01T077L	CAAGAGGCTGCTCCACAGGAA	01T077R	GACATCTTATTCAGAACTCTTG	01T077E	GGACATTAAGAGGTGATAGGTCTAGAGG	01T077A	AAACAGCAAGGAGAGCAACTGTT	01T077A
01T079L	01T079L	GATGGAGGCAACATCATCTCT	01T079R	ACAGCATGACAGTACAGACTT	01T079E	GGACATTAAGAGGTGATAGGTCTAGAGG	01T079A	CCCTCTACCTTAATCTCTTAAAGGTTCC	01T079A
01T083L	01T083L	CTCTTATCTGAGATGAGCCCT	01T083R	TCTGAGCTGTGATGTTGCCATTAC	01T083E	GGACATTAAGAGGTGATAGGTCTAGAGG	01T083A	TCGATAATCTAGTAAAGTCCCAAGTAAAGTCC	01T083A
01T084L	01T084L	CAAGGAGCAAAATCTGTATGAT	01T084R	CTGAAGCTCTCTGCAATTAAC	01T084E	CTACTTATAGGTGATAGGTGATGCAATTC	01T084A	TGATTAATGAGTCTCTAGTCTATTAAGTAA	01T084A
01T087L	01T087L	TCTCAGAGCTCTGCTCCAGCTGC	01T087R	TCCCAAGCCCTCAGGCTTAA	01T087E	GCATCTGCTCTCTCTGACCCAGG	01T087A	CCCTGGGTGAGGAGGCGCAGATG	01T087A
01T088L	01T088L	CAACCCCAAGACTCCCAAGGACAT	01T088R	TGCTGCTGCTATCTATCTAGGCG	01T088E	TGCTACCAACCCCAAGGCTCTCTCT	01T088A	AAGGAGGGGCTCTGGGTGATGCA	01T088A
01T089L	01T089L	ATTACATGCAATTAATCCACG	01T089R	GTTCCTCAGTCTCTGCTCCAC	01T089E	CAGTGAATAGACTGAGACCTAGAGAGC	01T089A	GCCTCTCTAGGTTCTGCTACTCACTG	01T089A

Table II

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')
01T090L	01T090L	CAGCATGTTTAAATGCTATATGA	01T090K	GATCCACATGGTTCACTTAC	01T090E	CTTTCTGACCACACAAATTTAAATGTAA	01T090A	TTACAAATTTTAAATTTGTTGGTTCAGGAAGG
01T091L	01T091L	ATTGGAGCCATTAATAATCTATCTAA	01T091R	TACCTGTGTTTAAATCTGCAAGTAT	01T091E	CATATAATTTTATCTCTCTGCGCCACAA	01T091A	TTGTGGCCACAGAGTAAATCAATATATG
01T094L	01T094L	TGGAATGCTCCCAAGTGA	01T094R	TACCTGTGTTTAAATCTGCAAGTAT	01T094E	GCAACATGGCTATCTAGGAGCATTC	01T094A	GCATCTCCCTCCCTATGAGCCATGTTGC
01T096L	01T096L	TCAGTGCAGAAATGTTGGCTTA	01T096R	TGGTCCCTATGAGGACATCTAGT	01T096E	CGACTCCCTTAAATGTGGAGCTCAGACACT	01T096A	AGTGTCTGAGCTCCACATTAAGGAGTGC
01T097L	01T097L	CAGGCTGCTCTTCTGTTAGAGCGC	01T097R	ACGTCTGCTGCTGTTAGAGCATATAT	01T097E	GTCTGCTGCTGCTGTTGGTGGCCG	01T097A	CGCGGACCCCAAGGAACGAGAAC
01T098L	01T098L	GGCCAGGTATAATACACTGGTAG	01T098R	ACTGAGCCACAGAGCGCATATGAC	01T098E	GTGACGCTGGAAGCTGGAACCCCAA	01T098A	TTGGGTTCCAGTCCACGCTGAC
01T099L	01T099L	CCATGCTGTTCTCCAGGCAAT	01T099R	TGTTAATTAATCTCCAGCCATCAG	01T099E	TGCTGCAATATACTACTCTCTGCGCT	01T099A	AGGCCAGGAGTAGTATGTGAGGCA
01T102L	01T102L	AGAGCCAGGTATCAAAAGTA	01T102R	CTCCCATCACTCTCTCAGCCT	01T102E	CTTGAGCAACCGCTGCTGCTTTA	01T102A	TAAACACAGCCAGCGTGGCTAGG
01T103L	01T103L	CAGAGGTATCAGACAGCTT	01T103R	ATCTGGCTCTCTCTGGAGTAT	01T103E	GCTTCTATAAGAGGTGAGTATGATATGTC	01T103A	GCATTAATTAATCACTCTCTCTTATAGAAC
01T104L	01T104L	CTGGAGAGAGCTGTTCAAA	01T104R	ACATTAATGAGAAAGCTGTTGA	01T104E	GAGCATTAATTTAGTATGTTATTTCTC	01T104A	GAGATAAAATCACTTAAACAGCAATCTC
01T105L	01T105L	AAATGCTGCACTGGCCCTC	01T105R	GAGGCCACAGATCAGAGAAC	01T105E	CTCTGCTCCCTTGAATGCCAAACAAAC	01T105A	GTTTGTGGCATCAGGGGACAGAG
01T108L	01T108L	GGATGAGGAAGAAACAGCCGT	01T108R	TTCAATCTGCTGATCTTCCG	01T108E	GAAGTAATGGAATGTGAGAAAGCCCT	01T108A	AGAGGCTTTCTGACCATTTCAATTCAC
01T109L	01T109L	CATTGTGCTGTTCTCCCTC	01T109R	TGAATCGTATGAACCTTAC	01T109E	CAAGCTACATGCTGCAAGCTTGTAC	01T109A	GGTACACCACTTGAAGATGTAGCTG
01T111L	01T111L	GGCTATTGATGGAATGTA	01T111R	ATACACATTTCTCATGTGTGTA	01T111E	GTGTGAGAGTAAATTAACATTTAAGATG	01T111A	CCATCTTAAATGTATTTATCTCTCACAAC
01T117L	01T117L	GTCTCCATCTCTTAAAGGAAAA	01T117R	CTTTATTTTAAAGTCTTGTGACAG	01T117E	GCACATGATTAATTAATATAGCTTTTC	01T117A	GGAAAGCTATTAATTAATATATCATGTC
01T118L	01T118L	TGCCAATCTTCTGGCAAAATCAA	01T118R	TTATGATGGAGATGTTGCTA	01T118E	AATGCTTCAACCCAGGGAAGCAG	01T118A	CTGCTCCCTGGGTTTGAAGCAAT
01T119L	01T119L	GCCAGAGCTGATGGAGTGAAC	01T119R	TGCTTTTAAATCTCAACAT	01T119E	GGCAATATAGCAAGACCCCATTC	01T119A	GAATGGGCTTCTGCTATATGGCC
01T120L	01T120L	CTTAAATCCCAATGCTTGG	01T120R	TACAGGAGCTGCCACCACTCTG	01T120E	CTCAGGCTGCTGCTTGTATGTTGTC	01T120A	GACAAATAAAGACAGCCGCTGAG
01T121L	01T121L	GAGGAGCTGATGAGGAGATCA	01T121R	GGCCAGTATTCGCCCTCTA	01T121E	CTCAGGCTGCTGCTTGTATGTTGTC	01T121A	AGGTGAGACCAACCCCAACCCA
01T128L	01T128L	TCCAGAGGCTCTCTGCTGCTG	01T128R	GTCCAGAGGAGGAGGCGCTG	01T128E	CATGTGAGAGGACAGCTCTCCCATC	01T128A	GATGGAGGCTCTGCTCTCTCAGATG
01T129L	01T129L	ACCATAATGCCAGTTAATCTGAC	01T129R	GGGAGCTGTGTCACACAGCTTAA	01T129E	CAAGCTCTTCCCTCACTTAACTGTTC	01T129A	GACAGTGTGTTGGGGGAAAGGTCTGG
01T131L	01T131L	CCCTGTTATTTCCAGATAATCAG	01T131R	CTCTGATCTGACCAAGCTAGGTA	01T131E	CAGTCACTGCTCTCTCACAACGATTA	01T131A	TTACTGGTGTGAGTAACAGCTGCTG
01T133L	01T133L	AATCTACCAATGTGACAAAGGC	01T133R	TCTTTTGAAGATGTCTGTTCTG	01T133E	TAAACAAATTAACAGAAACAAACAA	01T133A	TGTTGTTTTTCTTGTAAATTTGTTAA
01T135L	01T135L	TAAAGCTTTTATGCTTCCAC	01T135R	AGGAATAGATGATGTTGTTCTG	01T135E	GTCACTAGCACTTACAAATAATCTGATA	01T135A	TATCAGATTAATTTGTAATGGCTGAGTAC
01T137L	01T137L	AAAAGGAAGCAACCTCTCTA	01T137R	AATGGAATCTCACTGCTGTTA	01T137E	CTTCCCTGAGAGAGCTGTTGTA	01T137A	TACCAAGCTCTCCAGCGGGAAG
01T138L	01T138L	GAAATGATCACCAATTC	01T138R	AATACCAAGTCTCAGGTAGTATC	01T138E	GAGATGAGTAAATACACCAACCTC	01T138A	GAGGGTGTGTTATAGTCCATCTCTC
01T145L	01T145L	GGCAGCTGAGGTTAAGCATCTAA	01T145R	CAGCAGAGCTGGGATGATCTGGA	01T145E	CTTGAAACCAACATTAAGAAAGCCAC	01T145A	TGCGCTTTCTATGTTGGTGTTCAGG
01T146L	01T146L	GTGTGAGCTCCCACTGTA	01T146R	AGGAATGATGATGATGATCTGCTG	01T146E	GCAGACCAATGAGCTGAGGAGA	01T146A	TCTCAGTACCTGCTTATGCTGCTG
01T147L	01T147L	AATATGATGAGCTGATGAAAC	01T147R	TGTGCTGATGATGATGATGATGAT	01T147E	CATTAAGTATGATGATGATGATGATG	01T147A	TGGCAAGTACTGATGATGATGATGATG
01T148L	01T148L	AGGAAGGATATAGAGAACTTCA	01T148R	TCTTGATGATGATGATGATGATG	01T148E	GAAATGATGATGATGATGATGATG	01T148A	GACTTCAATGAGCCATGATGATGATG
01T150L	01T150L	TCAGAGAAATCGTTGAGCCTGG	01T150R	TTTATGAGTATGATGATGATGATG	01T150E	TGTGCCAGGCCAGGAGTGTGATG	01T150A	CCATTACACTCTGGCTGGGCAACA
01T151L	01T151L	GTACATGGGCTCTTTATC	01T151R	GGCCAGGAGCCAGAGGAA	01T151E	CCCTGTTGTTGTCAGCCCTAGGGA	01T151A	TCCATAGCTGACACACACACAGG
01T152L	01T152L	TCTCTAAGCTCATCTGCTG	01T152R	ACAAATTTTAAACTCTCTTGGGA	01T152E	AQAAAGTCTTGTGAAAGGCTGCTG	01T152A	CAGGTACCTCTTTTCAAGACTTTCT
01T153L	01T153L	ACTGATATGCTCCAGTAT	01T153R	GAGTGCAGACAGGATTCAT	01T153E	TTTATATGCTCTTTTATGCTATTAACATA	01T153A	TATGTTTATATAGCATAAAGGCAATATAA
01T154L	01T154L	CCATTTCTCCGTTTAAATA	01T154R	TCTCTTGGGTCAGTGTCTTTA	01T154E	GAAATATGATTAATGTTTCAACTAAATCG	01T154A	CGATTATGTTGAAACACATTAATATATTC
01T155L	01T155L	GGATAACCTGATGAATTCAC	01T155R	AGGGGATGGTGAATCTG	01T155E	CTGAGTATCCATTTCTATCTGCTTATCAA	01T155A	TGAAATAGCAGATAAGGAATGGATCTCAG
01T156L	01T156L	TCTCTCCCTGCTGTTGGGCTT	01T156R	GAGCAATCATTTGACAAACT	01T156E	ACTGGCTGATGATGATGATGATG	01T156A	CCAATCAATTCATCAGGCTCACT
01T157L	01T157L	AGCATGCTGATTTTCACTG	01T157R	TATACCATGATGATGATGATGATG	01T157E	GAATGATGATGATGATGATGATGATG	01T157A	TGCTCTCTCTCTCTCTCTCTCTCTCTCT
01T159L	01T159L	GTGAGTATTTGGCTCTCTG	01T159R	ACTTCCCTCTGAGAGCTT	01T159E	CCTCAGTAAATGTTGGCATTAATAAGTT	01T159A	AACTTTAATAGCCACAAATTAATAGTGG
01T160L	01T160L	CCCTATGTCACCAAACT	01T160R	ATATTTTGAAGGCAACAG	01T160E	AGATCAAAATTTATTAAGTAAATAAATA	01T160A	TTTTAGTTATTAAGTTTAAATTAATTTGATCT
01T162L	01T162L	AATAGGTTTGAAGGGAATAG	01T162R	TCATTAAATATCTCTGCA	01T162E	GAAACAAATTAAGTCTGATGATGATGATG	01T162A	AGCATAGTATTAATTAAGGACTAAATTTGTTTC
01T164L	01T164L	TAACTGTTCACTGATGATG	01T164R	TGAAGAGAAAGCTTGAAGGAGT	01T164E	GGCAGTTCATAGTTCACAGCTCTGAGA	01T164A	TCTGAGGCTCTGAGCTTATGAGCTG
01T166L	01T166L	ACAAATTTCTTCCATGATG	01T166R	TCCATACATAGTATGATGATG	01T166E	ATTATATGATCTCTCTCTCTCTCTCTCT	01T166A	GGCATTTTAAAGAGGAGGATCAATTAAT
01T167L	01T167L	CAAAATTTTAAATGCTCTGCTG	01T167R	AATAGAACTCAAGGAGTACAG	01T167E	CCGCTTATGATGTTGTTGTTGTTGTTG	01T167A	CAATAAATTAACAACTAAAGGCGG
01T169L	01T169L	CATACACCTCCCAAGCTAA	01T169R	TTGACTGTAATGATGATGATG	01T169E	GGAGATCAAAATCTCTACTAGCACTAACA	01T169A	TGTTATGTTGATGATGATGATGATGATG
01T171L	01T171L	GCAGAGGATGAAGAGGAGGAGTGGC	01T171R	TCTGTTTCACTCTGAGGATTAAT	01T171E	AGAGCTGTTTCACTCTGAGGCTG	01T171A	CAGCCATGATGATGATGATGATGATG
01T173L	01T173L	ACATCCAGGCTGATGATGCTG	01T173R	TCTGTTTCACTCTGAGGATTAAT	01T173E	TGCTGATGATGATGATGATGATGATG	01T173A	CCACACTGCTCTGTCAGCTGCA
01T175L	01T175L	TTATAGAGATCCCAATGAGGATG	01T175R	ATTACTGTGGTGCACAAAT	01T175E	CACAAATTAAGAACTCTCTGCTGGA	01T175A	TCAGCAGAAAGGATGCTTAATTTG
01T176L	01T176L	AGAGAGTCACTGATGATGCTCC	01T176R	AATACGCACTCTGTAATAA	01T176E	GAGTACTGTTGATGAGGAGCTCTAAG	01T176A	CTTATGAGCTCTCTCTCTCTCTCTCTCT
01T178L	01T178L	CAGTGAGCAATTAATCTAT	01T178R	AGTGAATGAACCCAGTCACTAGT	01T178E	TGGGGGCTGTTGTTGCAAGTGGC	01T178A	GCCATCTGAGCAACCCCTCCAA
01T179L	01T179L	CCTGTTAATAGCACTACCTCTT	01T179R	CATCAGAAATGATGATGATGATG	01T179E	CTGTTGATCACTCTCTCTCTCTCTCT	01T179A	CCATTAATGAAACTAGGATGATGATG
01T180L	01T180L	TACCAGATTTGAGGCTCAATATCTA	01T180R	ACATAACAAAGTGTGTTGTTGCT	01T180E	CTTCTGAGCTGGGAGTGTGCAATCC	01T180A	GGATTCTACTCTCTCTCTCTCTCTCT

Table II

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')
01T182L	01T182L	CATGCTTTTGTACAGAGGCAATTC	01T182R	AGTGTCTCAAGTGAAGAGACAA	01T182E	GGCTCTCCAAAAGAGCTATCACTCTCT	01T182A	AGGAAGTGTATAGCTCTTTTGGGAGACGC
01T184L	01T184L	ACCCAGCTACGGCATGCGAC	01T184R	TCCATTCACCTGAATATCCATTC	01T184E	CTCCACTGGCAGCTCCCACTATG	01T184A	CATAGTGGGAOCTTGGCCAGTCCAG
01T185L	01T185L	TTCAATTTGTAGATCTGCCCCCTC	01T185R	CTAATGGGAGTCCATCTCTCT	01T185E	TCATTTGGCAGCTGGGTTCGATGGCC	01T185A	CCCAATCGAACCCAGTGGCAATAGA
01T187L	01T187L	GTGCAATGTGCTGCTGCTGCTT	01T187R	CTCCCAAGAAAGAACTCACTCT	01T187E	CTTAAGCTATCGATCCACCCACTGG	01T187A	CCAGTGGGTGGATCGATAGCTTATGG
01T188L	01T188L	TAAAGCTGAACAGTAACCTCTTC	01T188R	TGAATTTGTGGCTTGACAAA	01T188E	GGCTGGGTATAGATTTTGGCACTA	01T188A	TAGTCCCAAACTCTATGACCCAGGCC
01T189L	01T189L	CAAAGATGCTGCTATTGAC	01T189R	CAGATGCTGCTCTCTATCC	01T189E	GGCAAGGTTCTGCTTAAGAAATCTTT	01T189A	AAAGAAATTTCTAGACGAACACTTGCC
01T192L	01T192L	AAACATTTAGAGGCAAGT	01T192R	TAAATTTGAAGCTCAACAGCCG	01T192E	CCGCAATCTATCTATGAAGATATGCG	01T192A	GCTAAATGCTTATGAAGATAGATCTGG
01T194L	01T194L	AGAAGCTTGAAGCAGCAGATTC	01T194R	TCTTGAATTTGGCAATGGCTTG	01T194E	AGCAATGGCAAGCTAGGAGAGATA	01T194A	TATCTCTCAGGTGCTTCATGCT
01T195L	01T195L	TAAAGGAGTGGCTGTTCAAT	01T195R	CTTACATGAATTTATGCTCTCAT	01T195E	CACATTTCCAAAGATACATCTATTAAGA	01T195A	TCTTAAATTTATGATTTTGGAAAGTGG
01T196L	01T196L	TGCAAAATCTTGATGCTT	01T196R	ATCTCTGCTATGGAGTATG	01T196E	TGAGAAATATTTGCTTTAATAAGCTGTT	01T196A	AAACAGGTTTATACAGCAAAATCTCTAC
01T200L	01T200L	TTTACATGATGATGACCAACA	01T200R	GTCTAGGCTGGGGATATATAG	01T200E	CATCATAGATTAAGGCCAAATATGCA	01T200A	TGCATATTTGGCCTTAATCTCTATGATG
01T202L	01T202L	CTTTTCAATGATGCTGCTATC	01T202R	CTGCTTTATCCACTTTGATATC	01T202E	CTCTCACTTTAACAATATGATGAGATA	01T202A	AAATGATTAAGGAAATAGCTGTTAAGCA
01T205L	01T205L	AGTGGCTTCAAGATCTCTT	01T205R	GCCAGATAGCTGCAATAGTATATA	01T205E	TTTGTCTTGAATTCACAGATTTAAT	01T205A	AATTAACCTGTGAATCCAAAGACAAA
01T206L	01T206L	AGATGCTGACCAAGCTTAAACT	01T206R	TGAGCTGTTGAGCCACTCT	01T206E	TAACTCAAACTGAGGAAGGCCCA	01T206A	TGCCCTCTCTCAGTTTCTTATTA
01T207L	01T207L	TGGCTATTTTGTGATCAAAAT	01T207R	ACTGCTGAGCAATGACATCTCT	01T207E	TCCTGTGATCACAGGACTATTAATCT	01T207A	AGATTAATATAGTCCGTGTGATCAAGGA
01T208L	01T208L	AATCGAGAGCAATCTCTAGT	01T208R	TGCCAAAGCAAGCACTTCAAT	01T208E	AATAGAACAGTTAATCAATTAAGCTGCG	01T208A	GCAGTCAAGTTAATGAATTAATCTTTCTAT
01T209L	01T209L	AGATTAATGATGATGCTGCTA	01T209R	AATTTCTCACGTGTGACTCA	01T209E	TCACCAAGAACTTATAGATCTGTTCTCT	01T209A	AGAGAAACAGATCTCTAAGTTCTGTGGA
01T211L	01T211L	ACCGAGAGGATGGAACAT	01T211R	TGCCAAGACTTTGACGGCTTA	01T211E	GATGTGTAGCTATTAATGTTTCTAGGCTA	01T211A	TAGCTTAAGAAACAAATACGTCTACACATC
01T217L	01T217L	TAAATGAGAAATGACCAATG	01T217R	CTCAGGAGCAATATCTTG	01T217E	GGCATAAGAGATTAATTAATTAATCTCTCA	01T217A	TGAGAGTTAATAATAATATCTCTATGGGC
01T220L	01T220L	ATTTTCTTCAATCACTGCTTCT	01T220R	GCTATGCTGATATCAAACTCT	01T220E	CTCTCAACCAAGAGTGTCAAACTAGAA	01T220A	TCTAGATTTTGTCACTCTGTTGTGATGAG
01T221L	01T221L	CCAAAGGAATGACATGTTT	01T221R	GCCTATGCTGATATCAAACTCT	01T221E	CCATCTTTATCTCTTAATAGGCCAC	01T221A	GCATTTGGAACCTCTACCTCTGGAAC
01T222L	01T222L	CTCTAGGCTTCAACATCTCACT	01T222R	ACACAGGATGAAATATGCTTA	01T222E	GCCTTATGCTCTTAATAGGCCAC	01T222A	GGTGGCTTAATGAGGATAAAGAAATGG
01T223L	01T223L	TAGGCACTTGCATCTGCTT	01T223R	AGAAATGCAATATGCTGCTG	01T223E	AACTTGAAGATTAATCTTTCTGAC	01T223A	TTGAACATTTCAAGTGTGCTTAAAG
01T224L	01T224L	CAAAAGCTAAAGGGGCTCT	01T224R	GATTCATGCAATATGCTGCTG	01T224E	GGCTTGAAGATTAATCTTTCTGAC	01T224A	TGACAGCAAGAAAGAAATATCTCAAGT
01T228L	01T228L	CGCTAAAGAGGAAAGGCTCTCT	01T228R	CAGGTCTCAGGATGTCAGACCT	01T228E	TGCCCTAGCACTCTGCTGCAACT	01T228A	AGTTGGCAGGATGCTCTAGGCCA
01T230L	01T230L	TGAATGTACCTTTAAATATGTTA	01T230R	CTCAGGAGCAAGAGGGA	01T230E	ATTTGTATGAAAGGCCCAAAAGAGG	01T230A	TAGTTTGTGCTCTTAACTCTGGCC
01T231L	01T231L	TTTTCAGGATGATATCTGCTCTA	01T231R	CAATCTGCCAGGCCCTCCCA	01T231E	AAATATAATATAGTCACTATATGGTACGTG	01T231A	CACTTTTGGCCCTCTCTTAACTCTGGCC
01T232L	01T232L	ACCAATGAAATAGATGACAGATG	01T232R	ATCCTTTGGATCACCTCAAAATA	01T232E	CCATAGGGTGTGAGGCAAGAAATTTG	01T232A	CAGTATGCCATATAGTGTACTATATATTT
01T233L	01T233L	GGGAGGTGCGAGGCGAGGGCA	01T233R	AAATGGTAAATAATTTGCTTA	01T233E	ATGGAAGACATATCTCTCTCTCT	01T233A	CAATTTCTGCCACTCACCTCTTGG
01T234L	01T234L	GGCTATGCTACAGTCTCTAGCTAA	01T234R	AAAGACCTGAAAGTCCCAAT	01T234E	CAGTGTGATGCTATGTTGTGCTCTC	01T234A	GGAGAGGATGAATGTGCTCTTCCAT
01T236L	01T236L	TCTCTGGGGGAACTGCTCTCAGTG	01T236R	TGCATATGCTCTCTCAACTCTCT	01T236E	GTGGCTCTGATCTAGGCTGTGAGCC	01T236A	GAAGACTCAACAATGCACTGCAACACTG
01T237L	01T237L	AAAGGCTATGAGGCTGCAACAA	01T237R	TGCCATATGCTCTGCTCCACACT	01T237E	GTGGCTCTGATCTAGGCTGTGAGCC	01T237A	GCCTCAAGCTAGATCAGAGGCCA
01T240L	01T240L	GGCTGAAAGGATGATGATTTTA	01T240R	TGGGTATATCAGCTGCTCAG	01T240E	GAGGCTCACAGGGGCCAGAGCTGA	01T240A	TCACCTCTGGCCCTGTGAGCCCTC
01T241L	01T241L	TGCTTATGTGCTCTTTTCACTC	01T241R	CATCTGATCTCTCTATACCTCA	01T241E	CAATATAGGCTGGAATAGTCTCTGACA	01T241A	AGGTTAGATTTTTTTTTTATGAAATAGCAAT
01T242L	01T242L	ATTGATCATCTCAATGCTA	01T242R	TGGTCCAATGAACTGGGCAAAA	01T242E	CAGTGGGCTGCTGCTATGCTCTCAT	01T242A	TGTAGATGAACATTAACAGCTCTATATG
01T244L	01T244L	TGAAGGAGCTGTCTCTCTGCTG	01T244R	GAAGGCTGAGCTGTGAGGATCAG	01T244E	CAGTGGGCTGCTGCTATGCTCTCAT	01T244A	ATGAGGCCATGCAAGCCCTCCACTG
01T246L	01T246L	CCTTCCCAATTAAGGACTCT	01T246R	GACATCTGCAATTTAGCCG	01T246E	GGCAAGATTTTTTAAAGACATGAAAG	01T246A	TGCAGAGATTAACGTATGCTGCTGAGTCC
01T247L	01T247L	AAGAAATGAAATGAAAAACAGTA	01T247R	TGAGTTTGGCATACCTTAGCAT	01T247E	ATAATGATGCAAGCTTAAGGAGGAG	01T247A	CTCCTCTTACCTTGGCATCTATAT
01T248L	01T248L	GTCTGGAGGCTCACTGGTAG	01T248R	ACGTACACATTAATCCCAAGT	01T248E	GTGATACATATAGCTTAAGGAGGAG	01T248A	ACCATGTTTGGCATAGCTCATATGTTATCAC
01T249L	01T249L	TGGCTCTACTTCAAAAGTCTT	01T249R	AAATCTGAAACCTGTGGA	01T249E	GTGATACATATAGCTTAAGGAGGAG	01T249A	CTTTCTATGCTTTTAAAAAATCTTCCC
01T250L	01T250L	ATACCATCTATCAAGAAAGCCG	01T250R	GGGCGGCGAGGGTAAAGTGTGA	01T250E	CTGTTTGTTCATTTGCTCTTAAACA	01T250A	TGTTTAAGGCAAAATGAAACAAACAGG
01T251L	01T251L	AAAGTGTATGCAATATGCG	01T251R	TCCAGCAAGTGTCTCTGGTAG	01T251E	CTGCTGATGCTCTATAGCTTGAATTTCT	01T251A	AGAAATCAAGAGCTAATAGCACTACCCAGG
01T253L	01T253L	TCCTCAGAAATCCCAACACC	01T253R	GGAAGACTGGCCCATGATTC	01T253E	GGCAAGATTTTTTAAAGACTTTCCACCA	01T253A	TTGCTGCAAAAGCTAATAGCACTACCCAGG
01T256L	01T256L	CTTTGTGTTAATGCTGAGCA	01T256R	AATCTTACTGTTCTGCAC	01T256E	TGCCCTCAGGAAATACAAAGAAAT	01T256A	ATCTTGTATCTCTCTGAGGCCA
01T257L	01T257L	CTACTGAGGAGAAAGCAATA	01T257R	ACACACTGCTCACTCTCG	01T257E	CCGCTGCTCTTAAAAAATCTCTTTA	01T257A	TAAAGATATTTTTTTTTTAAAGCTGAGCCG
01T258L	01T258L	CAGTAAGGATGAGGAGCACTAA	01T258R	ATTCGCACTGCACTCTCTG	01T258E	CCGCACTAAAAACCCGTAAGATGAA	01T258A	TTTACTCTACGGGTTTATGTTGGGG
01T259L	01T259L	TCAACTGTGACTTATATGAG	01T259R	CCTTAGGTGCTCTCTGGTA	01T259E	GCTCAGAGATTAAGTCTCTCCCTAGAAAG	01T259A	AGAGGTTTCTTGGGAGACTAATCTGAGC
01T262L	01T262L	AGAGGCACTTTCCCACTGGTTA	01T262R	TAGATTAAGGCTCTCTCTGTTA	01T262E	CACATACATCTATTAATGATGATCCAAAG	01T262A	CTTTGGTAACCTTATTAATGATGATGTTG
01T266L	01T266L	GCCTGAGACTGCTGCTAA	01T266R	TCTTCGCTGTGTTGTAAT	01T266E	CTAGAACACACAACTCCCACTCAAGTA	01T266A	TACTGTAAAGTGGATTTGTTGTTCTAG
01T267L	01T267L	TAGAACACACTGCTCCGCAAT	01T267R	AGCACTGGGGGCGGGGGGCAATG	01T267E	AAGAAATGAGGTTTCCACGCGGAGC	01T267A	GCCTCCGCGTGGAACTCTATCTT



SNP	Left Primer			Right Primer			Probes on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
01T268L	01T272L	CTGACTGCTCTCCCTCAACT	01T272R	TCAATAAATTTGGTAAAGTGGA	01T272E	GATCAAGCGCTTCCCACTTTTAAAGTAAT	01T272A	ATATCTTTAAAAATGGGAAAAGGCTTGATC	
01T270L	01T273L	GGGAGCTGTGCTTGCATACACG	01T273R	TTTAAATGCTCTGCTCTGACT	01T273E	GGAAGCCAAAATAGGAATAAATAAAGATC	01T273A	GATCTTTTATTTCTCTATTTTGGCTTCC	
01T271L	01T274L	CCAAATTTGAAGGACATATCTT	01T274R	TTCTCCCTATCTCTCCCTCA	01T274E	GCTGCTGATCTCGATGCTTCACAAAGGTAA	01T274A	TACCTTTGTGAAGCATCAAGATCAGCAGC	
	01T277L	CCGAAGCCCAAGAAGACGGCTGG	01T277R	GCCAGCAGTGTTCTTGCAAT	01T277E	CTGCGTACTGCTTCAATGAGGCCATAA	01T277A	TATTGGCTCTCTATGGAACATGCGCAGC	
	01T278L	GCTGGAATCAGGAAGATTTCTAAAGT	01T278R	CTCTCTCTGAAGTCTGTAGGAG	01T278E	CTTCTTAATGCTTAATGCTTTAGTTGATG	01T278A	CTACACTTAAGCAATAGCACTTAAGGAAG	
	01T279L	GCTTGCTGTGCTGCTCTCTCTGTC	01T279R	GTTTTCGCACTCGGGCTCTGGA	01T279E	CCACGCTCAAGGCTCTACAGAGGGGA	01T279A	TCCCCTCTCTAGGCTCTACGCTGAGG	
	01T281L	ACCATCAGATCTCATAGACT	01T281R	CTGTGCTCTACTCAAAATCTATCT	01T281E	CTCTATGATTAATTAACCTCCACCTGGTCC	01T281A	GGACCAAGTGGAGGTAAATTAATCATATAGAGG	
	01T282L	AGGACTGCCATTTCTCTAATCT	01T282R	TACAGATTCGGGACCAAAAAA	01T282E	AGAAATATAGGATAGGTGTAGAGATGG	01T282A	CACCTCTCTACACCTCTCTCTATCTCT	
	01T283L	ACGGCTTGCTGTGGCGAGGAACGA	01T283R	TCCCACCTCTGGGCTGGTCC	01T283E	CGGCGCGGAGAGCTGGCATGGT	01T283A	CAGCATCCAGCTCTCGCGCGCGCG	
	01T285L	GTAGAACATCAACCAATTAACACT	01T285R	CTCTCTAGAACCTCATATATGA	01T285E	GAACAGACTACTATACACCTAGAGACCA	01T285A	TGGGTCTCTAGGTGTATAGTAGTCTGTTC	
	01T286L	GGTTTATGCACTTCTCTCAAA	01T286R	CTAGGCGAGCTTCTCAATGAT	01T286E	CTGCTCTCAGCAACTTTCACCAATGAT	01T286A	AAATGTTGTAAAGGTGGTGAAGAGACG	
	01T287L	GGTTACAGAGTCTCCCAATCAAT	01T287R	TATACCTTCTCCCAATCTC	01T287E	CACAGAGAAGATAAATCTTTTCAGAAAT	01T287A	CTTCTGAAAAAGGTATTTATCTCTCTCG	
	01T288L	GTGAGCAATTCAGAGATCTTCTCA	01T288R	TATCCGCTTAATATAGAGCAATCT	01T288E	ATAAAATAGTAAGTAATTTTAAATAAGAGTT	01T288A	AACTCTATTTTAAATCACTTACTTATTTAT	
	01T290L	GTATGCTCTAATAAATCAATATCTCG	01T290R	GAATTCGCAATTTAAGCTGATTC	01T290E	CATATTCCTATTCGATAAAATATCTCTTAA	01T290A	TTAAGAGATATTTTATTCGATATGGAATATG	
	01T291L	CCCAATCAAAATGATACATCAACT	01T291R	TTCTCTATGCAAAATTAAGTACT	01T291E	CGAGCTGTATCTGTGTTCATCTCTTAA	01T291A	TAAAGGATGAACAACATACAAAGCTTCC	
	01T292L	ACTATCTGCTCTAAGGTGTGCAC	01T292R	GAATTAAGCTGGGCAATTAAGCTAA	01T292E	CCAGTGTAAATTTGGCTTGACAAGGT	01T292A	ACTTGTCTAGCCAATTTTCACCTTGG	
	01T295L	CTATGCTGCTCTTGTGCCAATTAC	01T295R	TGCAAGTGATTCAAAAGGGCTGTA	01T295E	GCATAGAAGCAGGACCCAAATTCAG	01T295A	CTGAATTTGGTCTGCTCTTCTTATCC	
	01T296L	ACCTGAAAGAGGAAGAAATCAAGT	01T296R	TGCAGCTGATACATAATTTCTT	01T296E	ATTCACTCACTATGGGCACTCTGG	01T296A	CCGAAGTCCCTCATCAGTGGTGAAT	
	01T298L	TTTCTGCTGTGCAAGCTAAAGAT	01T298R	TGCTATCTCATCTAGAAATCTAAGT	01T298E	TGCTTTAGTTGGTGAAGAAATGGTCAA	01T298A	TTGACATTTCTCTCAACTCAACATC	
	01T299L	ACATATACAGCTGTCCACAGCC	01T299R	TTTGATAGTAGTACGATTCACAC	01T299E	CCCACTCTGAACTTTTGTCTTTGGAGATA	01T299A	TATCTCAAAAGCAAAATGCTACAGGTGGG	
	01T300L	TCAGTGAGCCACAAATCCATCTCT	01T300R	GTTGTTTAAATCACTCACTCTGG	01T300E	GGGCTCTTATAGATCTGCTCTAAGAC	01T300A	CTCTTGAAGGAGCAATTAAGAGCCCC	
	01T301L	AATGTGGTGTCCACAGGTGTAG	01T301R	ATCCATGTGAATCTTCAATTTAT	01T301E	GTGTGGGAGGAGGAGGGGACGA	01T301A	TCTCTCTCTCTCTCTCCCACT	
	01T302L	GGAGCATTTTGTGGTATCTTTAT	01T302R	AACATAAAGCAAGCCAGCTTCA	01T302E	CGCTTGAAGTCTCTCAAGAAATAGAACA	01T302A	TGTCTATTTTCTTAGGAATGCACTGAAGC	
	01T303L	AGGATGCAAGCAGCGGGGCTGGC	01T303R	CTCTAGCACTAGCTGTCTGCT	01T303E	CGTGTGCGAGACTCTCTTATCTCT	01T303A	AAAGTAAAGGAAGTCTGGCCAGCAGC	
	01T305L	GAAGGCTGTGCAAGTGTAGAAC	01T305R	AGGCCATGCAATTAAGCTGAATAG	01T305E	CTGCTTATGATCAAGCTCTGACT	01T305A	AAAGTAAAGGAAGTCTGGCCAGCAGC	
	01T306L	AGGCTGAAATGGTGTCACTGA	01T306R	CAGCCATCAATGGTACAGT	01T306E	AGGCCAAAAGGCTGTGTGGAAGTCA	01T306A	TGACTTCCACACACCTTTTGGCTCT	
	01T307L	ACACTGTGAAATTTGTGGCCAAAT	01T307R	TTCTCTCAAACTCTGATCT	01T307E	GGTTTGTGCTGCTGCAAACTTGCA	01T307A	TTCGACCTTTCAGACTGAACAAACCC	
	01T308L	CACAGCAAAATATATATATGACA	01T308R	CACCATTCGCCCTGGCTGAAA	01T308E	GAAGAGTTTGTGTGGAAGAGCTGACA	01T308A	TTTCTCACGCTCTGCTGCGCAGGA	
	01T309L	AGAAGCCTCCAGGAACAC	01T309R	GTCTTTTCTCCAGTATAGGT	01T309E	CTCTGGCAGCAAGCTGTGAGAAA	01T309A	CTTGACACTCTCTACACAAACCTTTC	
	01T310L	GGCCCAATATGACCTCATCTTA	01T310R	ACCCTGGTAGGTGTATAGT	01T310E	CCCTCAAAGATATGAGTCTCAACCT	01T310A	AGGGTGTAGGACTTCAATATCTTTGAGGGG	
	01T312L	ACACTGTTGTGACATGGGG	01T312R	CCAGCAAAATGGAATTCAAATAT	01T312E	CCAAATGTCTCAAAATGTGTAG			

Table 11



[illegible]

Table II

Left Primer		Right Primer		Sequences (from 5' to 3')		Sequences (from 3' to 5')		Labeled Probe		Name		Sequences (from 5' to 3')		Sequences (from 3' to 5')		Name	
SNP	Name	SNP	Name	Sequence (from 5' to 3')	Sequence (from 3' to 5')	Sequence (from 5' to 3')	Sequence (from 3' to 5')	Sequence (from 5' to 3')	Sequence (from 3' to 5')	Sequence (from 5' to 3')	Sequence (from 3' to 5')	Sequence (from 5' to 3')	Sequence (from 3' to 5')	Sequence (from 5' to 3')	Sequence (from 3' to 5')	Sequence (from 5' to 3')	Sequence (from 3' to 5')
01T4251	GCCTTGTGAAGAAAGGAGTG	01T4251	CGTTATTTATGAAAACCTCCGAT	01T4258	CGTTATTTATGAAAACCTCCGAT	01T4258	GCTTAAACAGGGTTCAGACTACAGCTAC	01T4259	GTAGCTGTAGTCTGAACCTGTTTACC	01T4259	GTAGCTGTAGTCTGAACCTGTTTACC	01T4259	GTAGCTGTAGTCTGAACCTGTTTACC	01T4259	GTAGCTGTAGTCTGAACCTGTTTACC	01T4259	GTAGCTGTAGTCTGAACCTGTTTACC
01T4261	ATGCTGCTTCCCAAGGATACGAT	01T4261	AACACTGGTGGAACAACCCCAAGT	01T4268	AACACTGGTGGAACAACCCCAAGT	01T4268	AGTAAAGACGGGGTGTGGTGAGGTAC	01T4269	GTACCTCACCACCAACCCCTGCTTACT	01T4269	GTACCTCACCACCAACCCCTGCTTACT	01T4269	GTACCTCACCACCAACCCCTGCTTACT	01T4269	GTACCTCACCACCAACCCCTGCTTACT	01T4269	GTACCTCACCACCAACCCCTGCTTACT
01T4271	ACTCTCGCTCTCATCAACCAAGC	01T4271	TCCCTTAGTCTACACTCCCTCT	01T4278	TCCCTTAGTCTACACTCCCTCT	01T4278	CCCTTAGTCTAGATCTGCTGAATCCCC	01T4279	GGGGAATTCAGGATCTAGCTAGGAGG	01T4279	GGGGAATTCAGGATCTAGCTAGGAGG	01T4279	GGGGAATTCAGGATCTAGCTAGGAGG	01T4279	GGGGAATTCAGGATCTAGCTAGGAGG	01T4279	GGGGAATTCAGGATCTAGCTAGGAGG
01T4281	GGGTATATTCAGAGAGTCACTGGTA	01T4281	TGCCACAGTCCAGTCTATGCTAA	01T4288	TGCCACAGTCCAGTCTATGCTAA	01T4288	GCTTAAGATTTTCTGCCACTTAAGACAG	01T4289	GCCTTCTAGTCTGCTGCTGCTGCTG	01T4289	GCCTTCTAGTCTGCTGCTGCTGCTG	01T4289	GCCTTCTAGTCTGCTGCTGCTGCTG	01T4289	GCCTTCTAGTCTGCTGCTGCTGCTG	01T4289	GCCTTCTAGTCTGCTGCTGCTGCTG
01T4291	ACCCACATATTCATACCAACT	01T4291	TGCCACATTCATACCAACT	01T4298	TGCCACATTCATACCAACT	01T4298	TCATCTGAAACCTGCTGCTGCTGCTG	01T4299	TCATCTGAAACCTGCTGCTGCTGCTG	01T4299	TCATCTGAAACCTGCTGCTGCTGCTG	01T4299	TCATCTGAAACCTGCTGCTGCTGCTG	01T4299	TCATCTGAAACCTGCTGCTGCTGCTG	01T4299	TCATCTGAAACCTGCTGCTGCTGCTG
01T4301	TCAGTACGCAAAATATGACGCTGTA	01T4301	CGCGTCGAAGAGATGTAAGGTGGCAC	01T4308	CGCGTCGAAGAGATGTAAGGTGGCAC	01T4308	GCTCTGATATCTATGACACCAAGCTTAGAG	01T4309	GCTCTGATATCTATGACACCAAGCTTAGAG	01T4309	GCTCTGATATCTATGACACCAAGCTTAGAG	01T4309	GCTCTGATATCTATGACACCAAGCTTAGAG	01T4309	GCTCTGATATCTATGACACCAAGCTTAGAG	01T4309	GCTCTGATATCTATGACACCAAGCTTAGAG
01T4311	TGCTATTTTGTCTTACGTTGGCTTA	01T4311	TGCTATTTTGTCTTACGTTGGCTTA	01T4318	TGCTATTTTGTCTTACGTTGGCTTA	01T4318	CCTCATGTGGGATTCCTGTTGTGAACCTATA	01T4319	CCTCATGTGGGATTCCTGTTGTGAACCTATA	01T4319	CCTCATGTGGGATTCCTGTTGTGAACCTATA	01T4319	CCTCATGTGGGATTCCTGTTGTGAACCTATA	01T4319	CCTCATGTGGGATTCCTGTTGTGAACCTATA	01T4319	CCTCATGTGGGATTCCTGTTGTGAACCTATA
01T4321	GAGGGGCTATGGCCAGAGAGAC	01T4321	GAGGGGCTATGGCCAGAGAGAC	01T4328	GAGGGGCTATGGCCAGAGAGAC	01T4328	CCTCTTCCAGCGAGATTAAGGTAGT	01T4329	CCTCTTCCAGCGAGATTAAGGTAGT	01T4329	CCTCTTCCAGCGAGATTAAGGTAGT	01T4329	CCTCTTCCAGCGAGATTAAGGTAGT	01T4329	CCTCTTCCAGCGAGATTAAGGTAGT	01T4329	CCTCTTCCAGCGAGATTAAGGTAGT
01T4331	TCGTGCTAGACAGATGGGTAGTG	01T4331	TCGTGCTAGACAGATGGGTAGTG	01T4338	TCGTGCTAGACAGATGGGTAGTG	01T4338	ACCCTGAAGCAACCAATCCCGACACA	01T4339	ACCCTGAAGCAACCAATCCCGACACA	01T4339	ACCCTGAAGCAACCAATCCCGACACA	01T4339	ACCCTGAAGCAACCAATCCCGACACA	01T4339	ACCCTGAAGCAACCAATCCCGACACA	01T4339	ACCCTGAAGCAACCAATCCCGACACA
01T4341	CCCTCTTGCTCTGTAATCTCTTA	01T4341	CCCTCTTGCTCTGTAATCTCTTA	01T4348	CCCTCTTGCTCTGTAATCTCTTA	01T4348	GGAGTTAAGATCTGGAAGTCAAA	01T4349	GGAGTTAAGATCTGGAAGTCAAA	01T4349	GGAGTTAAGATCTGGAAGTCAAA	01T4349	GGAGTTAAGATCTGGAAGTCAAA	01T4349	GGAGTTAAGATCTGGAAGTCAAA	01T4349	GGAGTTAAGATCTGGAAGTCAAA
01T4351	AATGACAAATTCATAGCTTGGGCTT	01T4351	AATGACAAATTCATAGCTTGGGCTT	01T4358	AATGACAAATTCATAGCTTGGGCTT	01T4358	CTTCTACACTCTGTTTGAGACAA	01T4359	CTTCTACACTCTGTTTGAGACAA	01T4359	CTTCTACACTCTGTTTGAGACAA	01T4359	CTTCTACACTCTGTTTGAGACAA	01T4359	CTTCTACACTCTGTTTGAGACAA	01T4359	CTTCTACACTCTGTTTGAGACAA
01T4361	TCATCTCAAGCACTGAGTCTGCTT	01T4361	TCATCTCAAGCACTGAGTCTGCTT	01T4368	TCATCTCAAGCACTGAGTCTGCTT	01T4368	TAGTATTGATGTGGGCTGG	01T4369	TAGTATTGATGTGGGCTGG	01T4369	TAGTATTGATGTGGGCTGG	01T4369	TAGTATTGATGTGGGCTGG	01T4369	TAGTATTGATGTGGGCTGG	01T4369	TAGTATTGATGTGGGCTGG
01T4371	CCCTCGGTGTGAGTGTGGTCTGT	01T4371	CCCTCGGTGTGAGTGTGGTCTGT	01T4378	CCCTCGGTGTGAGTGTGGTCTGT	01T4378	GTGCTTGTGCTCTTCTTCTT	01T4379	GTGCTTGTGCTCTTCTTCTT	01T4379	GTGCTTGTGCTCTTCTTCTT	01T4379	GTGCTTGTGCTCTTCTTCTT	01T4379	GTGCTTGTGCTCTTCTTCTT	01T4379	GTGCTTGTGCTCTTCTTCTT
01T4381	CTGCTGGGCTCTCTCTCTTA	01T4381	CTGCTGGGCTCTCTCTCTTA	01T4388	CTGCTGGGCTCTCTCTCTTA	01T4388	AGCTGAGTCTGCTTCTTCTT	01T4389	AGCTGAGTCTGCTTCTTCTT	01T4389	AGCTGAG						

Table 11

Left Primer		Left Primer		Labeled Probe		Probe on Slide	
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
16-012L	GTCTGAGTCTGAGTATGTGAT	16-012R	TGTCATCATCTCTGTCCCTA	16-012E	ACCTGTCTTTTGTGGACATCTGCTTCTCT	16-012A	AGGAGAGCAGATGTCTCCAAAGACAGGT
16-013L	CTCTTCTCTCCCAAGTGGGA	16-013R	CATCCCAAACTACAGAGATCG	16-013E	AGACTCTGCCACCCAGGTGTGGGCT	16-013A	AGCCACACCTGGGTGCCAGAGTCT
16-014L	ACATCTGTGGACTTGGACAA	16-014R	AGTGGTGGCCAGGGTTTGG	16-014E	AGAGCTGAGAAATATCTGCTACACACTA	16-014A	TAGTCTACGACAGATATTTCTACGCT
16-016L	CATCACCCTCCAGAGCTGGAG	16-016R	GTGATGTGGTGTCTGTGTGGT	16-016E	TGACACTAACTCAGGAGCAACCATGTG	16-016A	CATCTGGTACGTCTGAGTTAGTGTCA
16-017L	AAATCCAAAGCACTGAAGCGGGC	16-017R	AGCTGTGGTCCCATATATGGTAA	16-017E	GGTGTGGGAGGACAGAGATCTCGGT	16-017A	ACGACAGATCTCTGTCTCTCCCGACACC
16-018L	TAATCCAAAGCAAACTGAAGGCTAA	16-018R	TTAGTAGGAGAGAGTAGAGCG	16-018E	AAAGCTGAGTGACGATGATCTTAATTC	16-018A	GAATTAAGGAATCATGCTACTGACGCTT
SNP							
16-020L	TACCTGGACAGCCGATCTCTA	16-020R	AACGAGATGAGCTGCTTAATAGTA	16-020E	TTCTAGACTCTGGCTCTCTTTCCAGGCCAGG	16-020A	CCTGGCTGTGAAAGAGAGGACGAGTCTAGAA
16-021L	TCAGAGAAGGCTATTGGCG	16-021R	TTGTCTTTGATTTCTACTGTAGAC	16-021E	CTGTGTGGAAGGTGACCTGTCTTGTGGAA	16-021A	TTTCCACAGACAGTCCACCTTTTCCACAGAC
16-022L	GGATGTCATGTTTCCCAAC	16-022R	CATCACTGCTATCTCTAACTTGT	16-022E	AACATGATCTCTGCGAGGTCTAATAGTCT	16-022A	AGACTAATATGACCTCAGGTACATGATGT
16-023L	TTCTCTGTGACTTCTGGCAT	16-023R	TTGTGTGCAAAATTTGCCCTGTGA	16-023E	TTCATAGACAGCCCGTCTTACGACCT	16-023A	AGGCTGTGAGAAAGCGGGCTGTATGTAA
16-024L	AGCGGGTGTCTCTCATAGT	16-024R	GGAGGTGCAAAATTTGCCCTTAC	16-024E	ATTTAATGGAGACTGAATGTTGTGGATAC	16-024A	GTATCCACACCAATCATGCTCTCCATAAT
16-025L	ATCTGTCTCTGTCTACAC	16-025R	GTGAATGAGGCTTGGTGTGTGACA	16-025E	CATCTGGCACACCTTTCCACCCAGCT	16-025A	AGCTGGTGGAAAGGTGTGCCAGGTG
16-026L	TTCTCCATATAGGCAAAATG	16-026R	TGGAAATGATGAGGGGTAGTG	16-026E	GAATGTGCCCTTTGTGCAATCAAGCT	16-026A	CTGTGGACTCCCAAGAGGGACCAT
16-028L	TGCCCAAGGGCTTACCTAGT	16-028R	CTGTGGCTCTCCAGGAAGTCC	16-028E	GTCTGTGATGGACTGGATGAGCTGAAGTT	16-028A	AACTTCTACGCTATCCAGTCCATCAAGGAC
16-031L	TCCTCTCTAAATGTGTCAATG	16-031R	CAAGTGGGAAGAAAGAAATTTCT	16-031E	AAATTCGAAGTCTCTTCTTAAAGGACAGG	16-031A	CTGTGACACCAACCGATGCAATCTCTGG
16-032L	TGAGGCACTGTGTGAATCTT	16-032R	TTATACATATCAGAGCGGAA	16-032E	AAATTCGAAGTCTCTTCTTAAAGGACAGG	16-032A	CTGTGCTTAAAGAGAGCACTTGTGAATTT
16-033L	GCAATCTCTAGTAATGGCAT	16-033R	TGGAAGAAATTTTCCCTCAACAT	16-033E	GGGACAGGGCTTCACTTCTATGTGCTTA	16-033A	TAGCCACATAAAGATGAAGGCTCTGCTCC
16-035L	CAGCTCAACAGCTGTCCCT	16-035R	CTGTGTGGAGCTGTATGGAAC	16-035E	GTGGGGGAAACAAATTTCTGTGAACAGGC	16-035A	CTGTGTCTACGCAATTTGTTTCTCCCCAC
16-037L	ATGGGCGCATGGGCTTTTAC	16-037R	CGGCAAGAAAGAACTGTCT	16-037E	CTCTGCTGTGTGCCCTCTGCTGCA	16-037A	CTGTGCTACGCAATTTGTTTCTCCCCAC
16-038L	ACTCCCAAACTGGGTTCG	16-038R	GAATGAAGTCCGCGAGGTA	16-038E	CTCCACTCTGCAAGTGTGGTCTCTGGA	16-038A	TCCAGAGCAACAGACTCTGCTGATGTGGAG
16-039L	TTGCCCTCTGGAGTTTAAAGTGG	16-039R	TATTTCTTCACTGCTTAGAT	16-039E	TAGTATATCTGAAACGCTATTAATCTTCTG	16-039A	CAGATGAATAATTAATGTTTCTGATATACTA
16-040L	CATCTACAGGCTCTCTCGG	16-040R	ATGATGTGTGTGTCTGAG	16-040E	TGATGCTGAGATTAAGTGTGTGCTAT	16-040A	ATAGCAATCAATTAATATCTGACATCTCA
16-041L	GGGTGCCCTCTAAATATCT	16-041R	AATCTCACAATCTCTTAAGACT	16-041E	TCCCACTTCAATGATTAAGACAGCTTT	16-041A	AAAGCTCTCTAGTACTACTAAGTGGGA
16-043L	CACACTGAGGCAAGCACTCGG	16-043R	GCATAGCTGTGTCTATTTAC	16-043E	TATGCTTGGGACATGCATCTGCTGACA	16-043A	TGTAGACAGATACGATCTCCCAAGGGAT
16-044L	GCATAATCTTAGCACTGAGAC	16-044R	CGACTCCAGTCCGCGACGCG	16-044E	ACGACAAACGTCATGATATCAGCACCA	16-044A	TGGTGTGATTAACGATGAGTCTTGTCTG
16-045L	AGCGGCGCTCTCTGCAACGCA	16-045R	CGACTCCAGTCCGCGACGCG	16-045E	CCAGAGCTGTGTGTAAGAGCTTCTCG	16-045A	CGAGAAGCTTTTGAACACCAAGCTCTGG
16-046L	TCCAGACTCTGCGAGGCTTA	16-046R	ACTCTTTTAAATTTGAGATGG	16-046E	GGCGCACTCTGGCTCTGCTGCAACTC	16-046A	GAUTTTGCAATGACCCCAAGTCTCGGC
16-047L	GGTGAGGAGCTCGAGCGCTACGC	16-047R	AATGCATTTAGAGAAAGAACGCG	16-047E	GGCCCAATGTCAAAGGCTCTCTCATAC	16-047A	CTGTACAGTATTAATAGTATGGGATAGC
16-048L	AGCTACTGGATGCACTGGGTCCG	16-048R	TGGCCCTTACGTGGATCTGGTA	16-048E	GTCTCTCCCACTCTGCTCTTATACAGAC	16-048A	TAAATGGAAGATATGTGCAAGGTCTTTAA
16-050L	ATCAATTTCTGTCTGTATAGTA	16-050R	CTTGAACCATGTTTGCACCTTAC	16-050E	TTAAGACCTTGGCCACTTGTCTTCCATTA	16-050A	AAACTACTCACAGCTATAGCTGTAGTGT
16-051L	TGATCTCCCAAGCACTGCG	16-051R	ATCTCTCCCAACACAGATACGA	16-051E	ACCACTCAACTATAGCTGTGTGATGTT	16-051A	GAATTTACTCACAGGGCATAGCTTAGAGGG
16-052L	AAATCTGATTAAGAGCCCTCTGA	16-052R	GGTATTATTAAGAGCCCTCTGA	16-052E	CCCTCTCAAGCTATCGGCTGTCAATTC	16-052A	GAACAGTCTGTCTTCTAGTGAAGTATCTG
16-053L	CTCTCCCACTAGGACAGGCAT	16-053R	CAGTCTCCGATACCCATCATCT	16-053E	ACGTGCTCTCACTAGCACAGCATGCTC	16-053A	TGTGCTCTTAATAAGAACCAATTTCTGTCT
16-054L	CATCTATGCAACGAGGTGGT	16-054R	AACAAGTGTGCTTCTCTGGT	16-054E	GAAGAAGTATGGCTCTCATTAAGGACCA	16-054A	TGGCATTTGTATGAATATGCCATCTCAGC
16-055L	CTTCCGAGTCTGCGATGAGTGTTA	16-055R	CCAACACATGTGGGTCTAAG	16-055E	GCTGAGACTGGCATTTACTACAGATGCA	16-055A	TGGCACAGGCAATCTCTCAGAGGGGTC
16-056L	TGAGGGGTCTGTGCTTCTTCTCG	16-056R	GAATCTCCCAACGCTCTGAC	16-056E	GAACCTTGAGGATAGCTCTGTGTGCCA	16-056A	CTGTGGCTGGCTGGGAGAGGTGAGGC
16-057L	CTGGGCTCTCATCTCTCTCGC	16-057R	AAGGGGCACTGTADAAACCGGGCG	16-057E	GTCTCACTCTCCCAAGCCAGCCAGC	16-057A	GAGCTGTATAGCACACACCCCTGTGATAC
16-058L	CITTAGCCTCAGAGGTGTGATCTA	16-058R	CAAGTGAACCTCATCTGTATAGAC	16-058E	GAATGCTGTATAGACTTCAGGCTTGGCT	16-058A	AGGCAAGCTCTGAGGTCTATACAGAGTT
16-059L	GCTTCTGTGTGACTAGTCTCTAA	16-059R	ATGGGCGCTTAAAGGTGATCT	16-059E	AGAAGTAGCCACACCAAGAACAGACAC	16-059A	GTGCTCTTTTGTGTCTTGGCTGACTTCT
16-060L	CGGCAAACTCTAAATTTTAA	16-060R	TCCAGTCCCGAGGTTTGG	16-060E	CCAGATCACTGAATCTCTGCAAGGCAAGC	16-060A	CTGTGCTCTGACAGATCTAGTATCTGG
16-061L	GAGCCAATGCCCAGAAACAGTTA	16-061R	TTCTCTATAGCTACGCAACCCCGCC	16-061E	TCTCATATGGCATGGCCATGCTCTTCTAT	16-061A	ATGAAAGGCAATGGCCATGGCTAGATGAGA
16-062L	ACTTCTTCTTCTGTCTCTCT	16-062R	GAACCCAGCACTGTCTGAC	16-062E	GCTGGGACCCCTAGTTTAACCTCGGCC	16-062A	GGCGGGGTAACTATAGGGTCTCCAC
16-063L	CTTCAATGCTGGGCTCGGGGC	16-063R	ATCTCGACCCCTGTGAACCCGAT	16-063E	GGTGTGAGGCTCTTCCGACCCACAGAT	16-063A	GGTCTCTCAAGCCCAAGAGGAGGGG
16-064L	ATAAGTGAAATCCGCTAGAT	16-064R	TGTCTCTTACAGGAGCATCTGGAG	16-064E	CCCTCTCTTTGGGGCTGTGGAGATC	16-064A	GAITGTGCAAGCACTAGGAGCTAGGAG
16-065L	TTCTCTGTCTAAATATTTGGCTC	16-065R	AGGAAACCCCACTCTCCCAAC	16-065E	GTGCTACTCTTCTAGTCCGTGCGCAATC	16-065A	ATCTGTGCTCTGACAGCTCTACACC
16-066L	GTGACTCTTCCAGAGAGCTGCTTA	16-066R	GGAATGGACAAATTTCTACAGATCT	16-066E	GGTGTGAGGCTTCTGCGACCCAGAT	16-066A	ATCTGTGCTCTGCAAGAGCCCTGGG
16-067L	CCACTCTTCTCTGCTCTCA	16-067R	AGAGAGCTCTCTCTGAAATA	16-067E	GTCTGTGCAAGTCTCAAGCTAATTCA	16-067A	ATCTGTGCTCTGCAAGAGCCCTGGG
16-068L	ACCAAGCTTTTCCCGAGGGCTTA	16-068R	CATTGGGCAAGATATCTTGG	16-068E	GTCTGTGCAAGTCTCAAGCTAATTCA	16-068A	TGAAATAGCTTGTAGACTCTGTGACAAAC
16-069L	CCATAGCACTGTGCTGGAATA	16-069R	CATTGGGCAAGATATCTTGG	16-069E	GTCTGTGCAAGTCTCAAGCTAATTCA	16-069A	GGTGTGGAAGGTGAGGAGAGCTGAG
16-070L	CTCTCAAGCTCTCTGCACCTT	16-070R	CATGGAATACATGCCATAGGAG	16-070E	CTCAGGCTTCTCTCAAGCTCCCAACC	16-070A	GGTGTGGAAGGTGAGGAGAGCTGAG
16-071L	ACACTATATCACCTTATATCTTAA	16-071R	TGGAAGAGGACTGCGAGAGCTTA	16-071E	GTGAAGTGTGCAAGAGCCCAAGTTAG	16-071A	CTAAACTCTGGGCTCTGTGCAAACTCTTTC
16-072L	ACATGTTCTCTCCCACTA	16-072R	TGGAAGAGGACTGCGAGAGCTTA	16-072E	GTGAAGTGTGCAAGAGCCCAAGTTAG	16-072A	CTAAACTCTGGGCTCTGTGCAAACTCTTTC
16-073L	ACTGTGAGCTGAGGACAGCGAGTTCG	16-073R	GTGGAGCTGAGGACAGCGAGTTCG	16-073E	GGGCAATGCTCCAAATATCCCTTATGAGCACTG	16-073A	CAGTGTCTCTAAGGGAATTTTGGACATGCTC

Table II

Left Primer										Right Primer									
SNP	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')					
16-0751	16-0851	TTTAAK(R)C'AT'GAGHTTGTGGTA	16-0753R	GTGTGTCGCCATACACAGGGAT	16-0755E	TTAAGTTGTATTGCTGTCAATTGCAATCTGT	16-0757A	CAGATGCATTGACAGCAATAACAACTTAA	16-0759A	CAGATGCATTGACAGCAATAACAACTTAA	16-0761A	GGGTGACAGATGAGGGCTGTGAGAGACGAG	16-0763A	GGGTGACAGATGAGGGCTGTGAGAGACGAG					
16-0761	16-0861	TGACTCGGCTGAGGCTGTGGATCTCT	16-0766R	TTTCTCAAGAAATCCATCTCCGT	16-0767E	ACAGA'CTTCTTGACCACTCATCTGTGACCC	16-0771A	CGCTGACAGATGAGGGCTGTGAGAGACGAG	16-0773A	CGCTGACAGATGAGGGCTGTGAGAGACGAG	16-0775A	CGCTGACAGATGAGGGCTGTGAGAGACGAG	16-0777A	CGCTGACAGATGAGGGCTGTGAGAGACGAG					
16-0771	16-0871	CTTGGGGGAGGGGTGATCATGAT	16-0779R	TGAGAAGGCTATTGCTCTACCA	16-0781E	TGAGAAGGCTATTGCTCTACCA	16-0783A	TGAGAAGGCTATTGCTCTACCA	16-0785A	TGAGAAGGCTATTGCTCTACCA	16-0787A	TGAGAAGGCTATTGCTCTACCA	16-0789A	TGAGAAGGCTATTGCTCTACCA					
16-0781	16-0881	TATGAGAGATGAATCAGCAT	16-0791R	CTCCGGCAGGAGACCAAGATTC	16-0793E	CTCCGGCAGGAGACCAAGATTC	16-0795A	CTCCGGCAGGAGACCAAGATTC	16-0797A	CTCCGGCAGGAGACCAAGATTC	16-0799A	CTCCGGCAGGAGACCAAGATTC	16-0801A	CTCCGGCAGGAGACCAAGATTC					
16-0801	16-0891	ATCAAAAGCCCATAGCAAAATCT	16-0809R	CATTTTACGCTCTCTTGCGACAC	16-0811E	CATTTTACGCTCTCTTGCGACAC	16-0813A	CATTTTACGCTCTCTTGCGACAC	16-0815A	CATTTTACGCTCTCTTGCGACAC	16-0817A	CATTTTACGCTCTCTTGCGACAC	16-0819A	CATTTTACGCTCTCTTGCGACAC					
16-0811	16-0901	AGCTGTACAGCTGTGATCAAAACCG	16-0819R	CTGCTGCTTAATTCGAGGCTCC	16-0821E	CTGCTGCTTAATTCGAGGCTCC	16-0823A	CTGCTGCTTAATTCGAGGCTCC	16-0825A	CTGCTGCTTAATTCGAGGCTCC	16-0827A	CTGCTGCTTAATTCGAGGCTCC	16-0829A	CTGCTGCTTAATTCGAGGCTCC					
16-0821	16-0911	AAATTCAGGCTTTTCAACAACG																	
Left Primer										Right Primer									
SNP	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')					
16-0831	16-0851	AGGAATTCAGAGCTGAAAT	16-0853R	GCCAGCTCCAGGCTGAGATTC	16-0855E	TAAAGTTGGACAATATCTGTCTTTCTAG	16-0857A	CTAGAAAGAGCAAGATATTTGTCGAATCTTA	16-0859A	CTAGAAAGAGCAAGATATTTGTCGAATCTTA	16-0861A	CTAGAAAGAGCAAGATATTTGTCGAATCTTA	16-0863A	CTAGAAAGAGCAAGATATTTGTCGAATCTTA					
16-0841	16-0861	TGAGGCTGAGGCTGCTCCCTCCG	16-0866R	ACCTGCGACACCACTCTGG	16-0867E	GAGGTGCGACCTGGAATCTGTCCACCC	16-0869A	CGCTGCGACCTGGAATCTGTCCACCC	16-0871A	CGCTGCGACCTGGAATCTGTCCACCC	16-0873A	CGCTGCGACCTGGAATCTGTCCACCC	16-0875A	CGCTGCGACCTGGAATCTGTCCACCC					
16-0871	16-0871	CGAAGGAAAAGATGATCAAT	16-0879R	CAGGTGTTGGTTAAAGAT	16-0881E	CAGGTGTTGGTTAAAGAT	16-0883A	CAGGTGTTGGTTAAAGAT	16-0885A	CAGGTGTTGGTTAAAGAT	16-0887A	CAGGTGTTGGTTAAAGAT	16-0889A	CAGGTGTTGGTTAAAGAT					
16-0881	16-0881	ATCCGAGAGGTATGAGTGATC	16-0889R	GGAAATGCTGCTCACTCTGG	16-0891E	GGAAATGCTGCTCACTCTGG	16-0893A	GGAAATGCTGCTCACTCTGG	16-0895A	GGAAATGCTGCTCACTCTGG	16-0897A	GGAAATGCTGCTCACTCTGG	16-0899A	GGAAATGCTGCTCACTCTGG					
16-0891	16-0891	CATGACACTGATGAGAGGGCC	16-0899R	TTTGACAGTGGCTCTCCAGATGG	16-0901E	TTTGACAGTGGCTCTCCAGATGG	16-0903A	TTTGACAGTGGCTCTCCAGATGG	16-0905A	TTTGACAGTGGCTCTCCAGATGG	16-0907A	TTTGACAGTGGCTCTCCAGATGG	16-0909A	TTTGACAGTGGCTCTCCAGATGG					
16-0901	16-0901	GGATGGGGAGGTGGCCCTTA	16-0909R	TGAGGTGCAAGAGGACATC	16-0911E	TGAGGTGCAAGAGGACATC	16-0913A	TGAGGTGCAAGAGGACATC	16-0915A	TGAGGTGCAAGAGGACATC	16-0917A	TGAGGTGCAAGAGGACATC	16-0919A	TGAGGTGCAAGAGGACATC					
16-0911	16-0911	TTTGGGGACAGCAACCTGGC	16-0919R	GAAATTTGTACTACGGACCTT	16-0921E	GAAATTTGTACTACGGACCTT	16-0923A	GAAATTTGTACTACGGACCTT	16-0925A	GAAATTTGTACTACGGACCTT	16-0927A	GAAATTTGTACTACGGACCTT	16-0929A	GAAATTTGTACTACGGACCTT					
16-0921	16-0921	GTTCATGTGTCAATTAACCTGTATC	16-0929R	CCCTTTGACAGCAGCTTA	16-0931E	CCCTTTGACAGCAGCTTA	16-0933A	CCCTTTGACAGCAGCTTA	16-0935A	CCCTTTGACAGCAGCTTA	16-0937A	CCCTTTGACAGCAGCTTA	16-0939A	CCCTTTGACAGCAGCTTA					
16-0931	16-0931	CTACACCCCTCAAAATCAAT	16-0939R	AGTTATTTTTCACACCAAAAT	16-0941E	AGTTATTTTTCACACCAAAAT	16-0943A	AGTTATTTTTCACACCAAAAT	16-0945A	AGTTATTTTTCACACCAAAAT	16-0947A	AGTTATTTTTCACACCAAAAT	16-0949A	AGTTATTTTTCACACCAAAAT					
16-0941	16-0941	ATCCAGAAATATGACACAGCCCTTA	16-0949R	GTGCTGTTCTGTTGATTAAGT	16-0951E	GTGCTGTTCTGTTGATTAAGT	16-0953A	GTGCTGTTCTGTTGATTAAGT	16-0955A	GTGCTGTTCTGTTGATTAAGT	16-0957A	GTGCTGTTCTGTTGATTAAGT	16-0959A	GTGCTGTTCTGTTGATTAAGT					
16-0951	16-0951	AAAGGAAAGGACACATATGG	16-0959R	TGACAGCAGTCCAGAGATGGGG															

Page 8

Table 11



SNP		Left Primer		Right Primer		Labeled Probe		Probe on Slide	
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
16-131L	GCTTGGATTACTGTGTTAT	16-131R	GGCTGCTCTCGAAGTCCCAAC	16-131E	TCTGAAGCTTTTAAAGAAATACCTGAGGAG	16-131A	CCTCTCAGGTATTTCTTAAAGAGCTTCAGA	16-131A	CCTCTCAGGTATTTCTTAAAGAGCTTCAGA
16-132L	TTCCAGATTGTGTGATCT	16-132R	TCCTGGAGGAGAAATTGAC	16-132E	GTGGCATTCATTTGAATAGAGGGTGACAGC	16-132A	GCTCTCAGCTTCAATTCATTTGAATAGAGGAC	16-132A	GCTCTCAGCTTCAATTCATTTGAATAGAGGAC
16-133L	AGCCAGGTGATTTTTCATAGTAT	16-133R	ACATCATGTGTGTTTGAAT	16-133E	TAGCTCAGAGGATGAGGAGGGTGTGAT	16-133A	ATCAAAGGCTGCTTCTTCTTCTAGGACTA	16-133A	ATCAAAGGCTGCTTCTTCTTCTAGGACTA
16-134L	TGCTGCTCAGAGGTGCGCG	16-134R	TTGGCTCTCAGAGGTGCGCG	16-134E	TGCTGCTCAGAGGTGCGCG	16-134A	TTCCAAAGGCTGCTTCTTCTTCTAGGACTA	16-134A	TTCCAAAGGCTGCTTCTTCTTCTAGGACTA
16-136L	ACTGTTCATGAGAGTAT	16-136R	CTTACAGCAGGGGGTGGTGG	16-136E	CAGCTGTGTGATGAGTGTGATGATGATG	16-136A	TCATCTATGAGCAGTATTCACCAAGGCTG	16-136A	TCATCTATGAGCAGTATTCACCAAGGCTG
16-138L	GAGTCTCATGTCTCCTCTCT	16-138R	AGGAGGTCTAGGCTTACTTC	16-138E	CAATCTTTCAGAGCAGCCAGCCATCC	16-138A	GGGATGCTGGGGGTCTTTCAGAAATG	16-138A	GGGATGCTGGGGGTCTTTCAGAAATG
16-139L	CAGCTGTTAAAGAAATTCG	16-139R	ACCCAGCAGCCCTTACAT	16-139E	TGGGATTTGGCCCTGTTAGTGTAGGAG	16-139A	CTTCTCAGCTTACCAAGGAGCAAAATCCCA	16-139A	CTTCTCAGCTTACCAAGGAGCAAAATCCCA
16-140L	GAGACCTCTCTCTGCTGCTCA	16-140R	TTCTGGGCCACCAAGGGAACCC	16-140E	CAGGTCAAGATGTTTGTAGTCAAGATGTC	16-140A	GACATCTTGTACTCAAAACATCTCTGACCTG	16-140A	GACATCTTGTACTCAAAACATCTCTGACCTG
16-141L	GCTGACACTGCTCTCTCCGGCA	16-141R	TGGGAAACAGGGGCTTGGCATAG	16-141E	TGGCATAGTCTGTTTATAGACATGAGCTTG	16-141A	CAAGCTCATGCTTAAACAGGAGCTATGCCA	16-141A	CAAGCTCATGCTTAAACAGGAGCTATGCCA
16-142L	GGGTGGGAGGCTCTGGGTA	16-142R	GAAGCCGCTGCTGCTGTGCTGTC	16-142E	GCCTAGGGGAGGCTCTCAGCAGCCCA	16-142A	TGGGCTCTGAGGCTGCTGCTGCTGAGC	16-142A	TGGGCTCTGAGGCTGCTGCTGCTGAGC
16-143L	CATCACTCAGGACAAAGTCCCTCTG	16-143R	CAGAAGAGCCCTCTGCT	16-143E	GGCACCATCTTCTTCTAGAAATGGAATGCTG	16-143A	TTCTGCTCTCTAGAAATGGAATGCTGCTG	16-143A	TTCTGCTCTCTAGAAATGGAATGCTGCTG
16-145L	AGGCCAGCTCTGCTCAGAGCTA	16-145R	GGGTGAGCAGCCCTGGGCTG	16-145E	GTGTGGGATTCAGTCTCATTTCCTCTTA	16-145A	TAAAGGGAATGAGCTATTAATCCCAAGC	16-145A	TAAAGGGAATGAGCTATTAATCCCAAGC
16-146L	GGTGGGCTCAGAGGTGTTAGAG	16-146R	AGAGGTGGGAGGAGGGGCTTA	16-146E	CTGGCTGTTTGTAGTCTCAGGCTTACCTTTT	16-146A	GAAAGGTTTACCGGCTTAAACAGCCAG	16-146A	GAAAGGTTTACCGGCTTAAACAGCCAG
16-147L	GAAAGGTAGCAATTCCTCTCGG	16-147R	ATTCATGTCATCCCAACAACT	16-147E	TGAGGATCTCCAGTAAAGGAATGGTGTG	16-147A	CAACCATCTCTTACTGGGAGTATCTCTCA	16-147A	CAACCATCTCTTACTGGGAGTATCTCTCA
16-148L	AATTTTGGTTGGATCTGGGTA	16-148R	CTCTGACCATTTGGTGTGTTGTA	16-148E	GTATGCAATACCTCTCTGATATGCTCTGG	16-148A	CCAGAGCATTAATCAAGAGGATATCTATAC	16-148A	CCAGAGCATTAATCAAGAGGATATCTATAC
16-149L	TCAGAGCAAAAGCTGAGGATA	16-149R	CACCTATGATAGGACTTCACTAA	16-149E	TCAGTGTTCAGCAAAATGCTATGGAAGAG	16-149A	CTCTCTCTAGACATTTTGTGAAACATGTA	16-149A	CTCTCTCTAGACATTTTGTGAAACATGTA
16-150L	AGCCAGACTGACAACTGTA	16-150R	GAACGAGGAGGAGGAGGAGGAGG	16-150E	CCTGTATTGCTCAACATATCAGGTGAGG	16-150A	CCTCAGCTGATGTTTGTGAGGATTAATTC	16-150A	CCTCAGCTGATGTTTGTGAGGATTAATTC
16-151L	TTCCCGGACTCTCTGTTATC	16-151R	TGAACAGGAGGAGGAGGAGGAGG	16-151E	GAAGTAAACCTCTCAAGGAGGAGGAGG	16-151A	ATTCAGGCTTGGCTTGTGAGGATTAATTC	16-151A	ATTCAGGCTTGGCTTGTGAGGATTAATTC
16-152L	TGGGTACCTCTGGGAGGAGGAGG	16-152R	CAGGCCAGACTCTGCTCTCTATC	16-152E	CAGACCCAGGAGGAGGAGGAGG	16-152A	TCCTCTCTGAGCAATTTTGTGAAACATGTA	16-152A	TCCTCTCTGAGCAATTTTGTGAAACATGTA
16-153L	TCGGCAGCTCTACGCTTACCGGC	16-153R	CAGGCTGGGAGAGCTGCTG	16-153E	CGCGCATCTTCTAGCAGGATGAGGAGC	16-153A	GGCTTCCATCTCTCTAGGAAATGCGG	16-153A	GGCTTCCATCTCTCTAGGAAATGCGG
16-155L	TTTCCAGAGCTCTAGTCTGGGG	16-155R	TTCCAGAGCTCTAGTCTGGGG	16-155E	AGCCAAAGGAGGAGGAGGAGG	16-155A	TTGTGAGCAGTGGCTTCAAGAGTATGCTCA	16-155A	TTGTGAGCAGTGGCTTCAAGAGTATGCTCA
16-156L	CAGAGCTCTATAGCAGGAGCTAT	16-156R	AAGAGGCTGGGAGGAGGAGG	16-156E	AGCCAAAGGAGGAGGAGGAGG	16-156A	GCATCAGGCACTCTGCTCTGCTGCTG	16-156A	GCATCAGGCACTCTGCTCTGCTGCTG
16-157L	ACAGGTCAGGCTCTCTATG	16-157R	CTCCTGATGTAACCCCACTC	16-157E	TCACCTCAAGATCATCTCTCTTTAAC	16-157A	GGTTAAAGAGGAGCATGATCTGAGGTGGA	16-157A	GGTTAAAGAGGAGCATGATCTGAGGTGGA
16-158L	CTTAAGTCTCTCTCTCTGCTTCA	16-158R	ACCCATGCTGGGAGGAGGAGG	16-158E	TGGGATGTAAGGAGGAGGAGGAGG	16-158A	CTGCAATCTCCCATGCTGATGCTCA	16-158A	CTGCAATCTCCCATGCTGATGCTCA
16-159L	TGGCTCTAGAAATCTTCA	16-159R	CATCTCTCTGAGGAGGAGG	16-159E	TGGGATGTAAGGAGGAGGAGGAGG	16-159A	TGAGCAGCTGTTATCTTCTTACTACCA	16-159A	TGAGCAGCTGTTATCTTCTTACTACCA
16-160L	CTGCTCTTGTGCTACTAA	16-160R	CTCTGGGCAACCCAGGTA	16-160E	ATTTCACTCTGAGGAGGAGGAGG	16-160A	GAAGAGGAGGAGGAGGAGGAGGAGG	16-160A	GAAGAGGAGGAGGAGGAGGAGGAGG
16-161L	AAGCTCTAGGAGGAGGAGGAGG	16-161R	GGGCACTCTCCGAGGAGGAGG	16-161E	TGGAAATGAGGAGGAGGAGGAGG	16-161A	TCCAATGAGGAGGAGGAGGAGGAGG	16-161A	TCCAATGAGGAGGAGGAGGAGGAGG
16-162L	CAGAAAGGAGGAGGAGGAGG	16-162R	AGCAGAGGAGGAGGAGGAGG	16-162E	GGCAGGATGAGGAGGAGGAGGAGG	16-162A	GGTGGAGGAGGAGGAGGAGGAGGAGG	16-162A	GGTGGAGGAGGAGGAGGAGGAGGAGG
16-163L	TCCTCTCTCTCAGAGGAGGAGG	16-163R	CCCTCTCTCTCAGAGGAGGAGG	16-163E	TCGAGGAGGAGGAGGAGGAGGAGG	16-163A	TTGTGAGGAGGAGGAGGAGGAGGAGG	16-163A	TTGTGAGGAGGAGGAGGAGGAGGAGG
16-165L	TGATAATGTCACAGCTTTCG	16-165R	TGATGACTCAGTAAACCGA	16-165E	AGCAGGAGGAGGAGGAGGAGGAGG	16-165A	GGTGGAGGAGGAGGAGGAGGAGGAGG	16-165A	GGTGGAGGAGGAGGAGGAGGAGGAGG
16-166L	CCAGCAGGAGGAGGAGGAGGAGG	16-166R	AGCAGGAGGAGGAGGAGGAGG	16-166E	AGCAGGAGGAGGAGGAGGAGGAGG	16-166A	GGTGGAGGAGGAGGAGGAGGAGGAGG	16-166A	GGTGGAGGAGGAGGAGGAGGAGGAGG
16-167L	CTCCTCTCTGAGGAGGAGGAGG	16-167R	CCCAAGGAGGAGGAGGAGGAGG	16-167E	AGCAGGAGGAGGAGGAGGAGGAGG	16-167A	GGTGGAGGAGGAGGAGGAGGAGGAGG	16-167A	GGTGGAGGAGGAGGAGGAGGAGGAGG
16-168L	GGTCCAGGAGGAGGAGGAGGAGG	16-168R	TTGTCCAGGAGGAGGAGGAGGAGG	16-168E	CTGCTCTCTCAGGAGGAGGAGGAGG	16-168A	GGTGGAGGAGGAGGAGGAGGAGGAGG	16-168A	GGTGGAGGAGGAGGAGGAGGAGGAGG
16-169L	GTGAGGAGGAGGAGGAGGAGGAGG	16-169R	CTGATGCTCTCAGGAGGAGGAGG	16-169E	GGCATGGGAGGAGGAGGAGGAGGAGG	16-169A	CTGTTGGGAGGAGGAGGAGGAGGAGG	16-169A	CTGTTGGGAGGAGGAGGAGGAGGAGG
16-170L	ATGTTTATGTCACAGGAGGAGG	16-170R	ATGTTTATGTCACAGGAGGAGG	16-170E	CTCAGGAGGAGGAGGAGGAGGAGG	16-170A	CCGACAGGAGGAGGAGGAGGAGGAGG	16-170A	CCGACAGGAGGAGGAGGAGGAGGAGG
16-174L	GGGCTCTCTTATGAGGAGGAGGAGG	16-174R	AGATCCAGGAGGAGGAGGAGGAGG	16-174E	TTGAGTGAATGTAATCTCTCTCTCTG	16-174A	TCAGCAGGAGGAGGAGGAGGAGGAGG	16-174A	TCAGCAGGAGGAGGAGGAGGAGGAGG
16-175L	TTGCGCTCTCAGCAGGAGGAGG	16-175R	ACTCATTTTATGAGGAGGAGGAGG	16-175E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-175A	GCTGGAGGAGGAGGAGGAGGAGGAGG	16-175A	GCTGGAGGAGGAGGAGGAGGAGGAGG
16-176L	CCCTCTCAGTGGAGGAGGAGGAGG	16-176R	TTAGGAGGAGGAGGAGGAGGAGG	16-176E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-176A	CAAACAGGAGGAGGAGGAGGAGGAGG	16-176A	CAAACAGGAGGAGGAGGAGGAGGAGG
16-177L	GTATAATGATGAGGAGGAGGAGG	16-177R	TTTACAGGAGGAGGAGGAGGAGGAGG	16-177E	ACAAGAGGAGGAGGAGGAGGAGGAGG	16-177A	GAAGTGGAGGAGGAGGAGGAGGAGG	16-177A	GAAGTGGAGGAGGAGGAGGAGGAGG
16-178L	CAATCTAGAAAGGAGGAGGAGG	16-178R	CTCAGGAGGAGGAGGAGGAGGAGG	16-178E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-178A	GAAGTGGAGGAGGAGGAGGAGGAGG	16-178A	GAAGTGGAGGAGGAGGAGGAGGAGG
16-179L	TGAACATACGAGGAGGAGGAGG	16-179R	AGGAGGAGGAGGAGGAGGAGGAGG	16-179E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-179A	GAAGTGGAGGAGGAGGAGGAGGAGG	16-179A	GAAGTGGAGGAGGAGGAGGAGGAGG
16-180L	CCCATGAGACATGAGGAGGAGG	16-180R	CGGTGAGGAGGAGGAGGAGGAGGAGG	16-180E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-180A	GAAGTGGAGGAGGAGGAGGAGGAGG	16-180A	GAAGTGGAGGAGGAGGAGGAGGAGG
16-181L	AAGTAAAGATGAGGAGGAGGAGG	16-181R	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-181E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-181A	GAAGTGGAGGAGGAGGAGGAGGAGG	16-181A	GAAGTGGAGGAGGAGGAGGAGGAGG
16-182L	TTCTTGAAGGAGGAGGAGGAGG	16-182R	ATGGCTCTGAGGAGGAGGAGGAGG	16-182E	GAAGGAGGAGGAGGAGGAGGAGGAGG	16-182A	GAAGTGGAGGAGGAGGAGGAGGAGG	16-182A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-001L	TAGACTTACTGATGCTGCTG	20-001R	TTCTCTTCTGAGGAGGAGGAGGAGG	20-001E	ATGGCTCTGAGGAGGAGGAGGAGGAGG	20-001A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-001A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-003L	AGCACTTCCGAGGAGGAGGAGG	20-003R	CACAGTAAACAGCAATTTATC	20-003E	TTTATGAGGAGGAGGAGGAGGAGGAGG	20-003A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-003A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-005L	GAATCTCTCTGAGGAGGAGGAGG	20-005R	CCAGGAGGAGGAGGAGGAGGAGGAGG	20-005E	GAAGTGGAGGAGGAGGAGGAGGAGGAGG	20-005A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-005A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-007L	GAATACATGCTATCTGCTGAG	20-007R	TGACATTAATGAGGAGGAGGAGGAGG	20-007E	GAAGTGGAGGAGGAGGAGGAGGAGGAGG	20-007A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-007A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-008L	CAGGTGAGGAGGAGGAGGAGGAGG	20-008R	TGCTCTCAATATCCCAACAC	20-008E	GAAGTGGAGGAGGAGGAGGAGGAGGAGG	20-008A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-008A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-010L	GAATGAGGAGGAGGAGGAGGAGG	20-010R	AGGAGGAGGAGGAGGAGGAGGAGGAGG	20-010E	GAAGTGGAGGAGGAGGAGGAGGAGGAGG	20-010A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-010A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-011L	GAAGTGGAGGAGGAGGAGGAGG	20-011R	TAAAGGAGGAGGAGGAGGAGGAGG	20-011E	ATTCCTCTGAGGAGGAGGAGGAGGAGG	20-011A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-011A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-012L	GAAGTGGAGGAGGAGGAGGAGG	20-012R	GGTCTGGAGGAGGAGGAGGAGGAGG	20-012E	TTTCTCTCTGAGGAGGAGGAGGAGGAGG	20-012A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-012A	GAAGTGGAGGAGGAGGAGGAGGAGG
20-013L	CTGTGGAGGAGGAGGAGGAGGAGG	20-013R	TATCAGGAGGAGGAGGAGGAGGAGG	20-013E	TTTCTCTCTGAGGAGGAGGAGGAGGAGG	20-013A	GAAGTGGAGGAGGAGGAGGAGGAGG	20-013A	GAAGTGGAGGAGGAGGAGGAGGAGG

[illegible]

Table IV

[illegible]

Table II

SNP	Left Primer			Right Primer			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
22-008L	22-008L	CCCCAGGCTGACTCAGAGAGTTG	22-008R	GAGGCTTCTCTAGACACTGGC	22-008E	GGCTCGGTGGGTTTGCCTAGGGGA	22-008A	TCCCTCAGTGCAGAAACCCAGCGAGCC	
22-015L	22-015L	TTGGAACTCTTAATACACTTTCG	22-015R	TGTCACTGGGCCAAAATACATCTCAT	22-015E	GATTTCTGTCTGGGAGTCAAGATCCAG	22-015A	CTGATCTGAGATCTCCCAACAGCAAAATC	
22-016L	22-016L	CCCAATGTGAGGCTCTTGGGCAC	22-016R	CAAGCTATGCACTTAAGATTATG	22-016E	TCCAAATAGAGAGCCCAAGATGCTCATG	22-016A	CATGAGGAGCTCTGGGCTCTATCTTGA	
22-018L	22-018L	TCACTGATGGTCAATGCTGTGTC	22-018R	GTTCACTGTGTATACCCGTGA	22-018E	CATAAAGAAATTTGTCACAGTGAAGAAACAG	22-018A	CTGTTCTCTACTGTGTGACAAATTTCTTATG	
22-019L	22-019L	TCAAGAGAGCTGCTCTTCTCACAG	22-019R	GAGGGGCTCTTCTTCTCTTGGCCA	22-019E	GTACACACTCTCCAGAGTGGGGAATCTG	22-019A	CAGATTTCCCAACCTCTGGAGAGGTGTGAC	
22-020L	22-020L	TCAAGTGAATCTCTCTGCTCAAC	22-020R	GGGGCTGACATATGCAATTC	22-020E	AGAATCTTATATCAGAGTCAAGTCACTGG	22-020A	CCAGTGCATCTGACCTGATTAATGAGATTCT	
22-021L	22-021L	GAACTCAAACTCTTCTTATCTTCT	22-021R	AGCAGCTAGGCAAGTATGCCAGGTAT	22-021E	AGATGAGAACCAAGCTTAACCAACCCAGG	22-021A	CTGGGCTGGTTAGCCCTGGTCTCATCT	
22-023L	22-023L	GTGACGGCAGAGATCTCAACAC	22-023R	TGTTTCTCTTGGAAAGTGC	22-023E	CTCAACAGGAAATGGAAATCAAAATC	22-023A	GATTTTATTTTCTCAATCTCTGTGTGAG	
22-024L	22-024L	GGAGAGGATGCGGCAAGAGTTA	22-024R	AGGCAAGTGTCTCCAGGTTTAT	22-024E	TTCATATTAACAATATGAGCCAAACCA	22-024A	TGGTTGGCTCACAATTTGTGTAATATAA	
22-025L	22-025L	CAATCTTTCTTCTTCTTCAACAA	22-025R	GTATCCCACTTCCAGCTCTCTC	22-025E	ACAATGTCTCAACCACTACTGACTA	22-025A	TAGTCAGTAGTTGTGGCAGTACAGATTGT	
22-026L	22-026L	TATGTGTATGAGGTGTATACCTGTG	22-026R	GAATGCCATATATACCTCTCA	22-026E	CTCTAGTCTGCTCTCTCTTCTTCAATAGA	22-026A	TCTAATGGAAGAGAGAGCTAGACTGAGAG	
22-027L	22-027L	GAGCTGTGTTCTATGTTGGCAGTAG	22-027R	GATTTGAGAGACTTGTAGTTTCAAG	22-027E	AGACTTCTCTGTCTAGTATCAAAATTTATCAGC	22-027A	GTGTAATTAATTTGATCTAGCAGGGAGGTCT	
22-028L	22-028L	AGTAAGGTTAACTGTGACTCTCT	22-028R	CAGTTTACAGTGAATTTGCCAGTA	22-028E	CTTCACCTACCAATGTAATCTCTCATGGGCAA	22-028A	TTCCTCATAGTGGCTAGCACTATATGTGTAC	
22-029L	22-029L	CGGGGTTTCTTCCATGTTGGTC	22-029R	GGGGTCACTGTTTAAACCTTA	22-029E	TCCAAGCACTCGGCTGGCCAAAGG	22-029A	CTTGGCCACCCGAGAGTGTCTTGA	
22-030L	22-030L	TGGCTGATGTTAGAGTGGTGTAGCAT	22-030R	ACCAACGAGCTCTGCTGGAGCG	22-030E	GGGAGACTGTGGGTGTCTGTGCAAGCT	22-030A	AGGCTGCAGACAGCAACAGTCTCTCC	
22-031L	22-031L	CTGCTCTTCTCCCAAGATCA	22-031R	AGGCAAGTCTCCAAGCAGGGA	22-031E	CAGCCACACAGACTACTCTTCTTCAATGGA	22-031A	TCTCTGAAAGGAGTGTCTGTGTGTGCTG	
22-032L	22-032L	CATGGCAGAAATCAAGCACTT	22-032R	CCTAGTCTGAGCCGATCAG	22-032E	GTCTACTAGCACTACAGAACCATATGGG	22-032A	CCCATATGTTTCTGTAGGTGCTCAATGAC	
22-033L	22-033L	CTGGAGATAAGGCTCTAGATTTTAT	22-033R	GGACAGCAAAATGCTGTAAACA	22-033E	TATGACTTACATGTATGATGAAATTTTCA	22-033A	TGAACATTTCACTCATCATGTGATGATATA	
22-034L	22-034L	TTAGTATGCTCTCTTCTCACTCAG	22-034R	CTCAAGGCTCTTACATCTTAA	22-034E	TCTCAACTAGTATTTCTCACTAGGACAT	22-034A	ATGCTCTAGCTGAGATCACTAGTTGAGA	
22-035L	22-035L	TGATGGGTGTTTGGAGTTTGACAA	22-035R	TGCTCTTGTGTTCTCACT	22-035E	AACACTATGTTAGGCGCTTTGATCTCA	22-035A	TGGATCAAAAGGCGCTTAACATGATGTT	
22-036L	22-036L	CAAGATGTAGAGGCACTGTGCTTA	22-036R	TTCAAGGCTGAAATTTCAATGTA	22-036E	TGAATAAACAGCAAGCAAGCGCTGTGGTTC	22-036A	GAACCCAGGCTCTCTTTTGTATTTATCA	
22-037L	22-037L	AGCCCACTACTGACAGTCAATC	22-037R	ACTGTCTCACTCTGAAATGTGAAAT	22-037E	CAAGTACTTAATCACTAGTACAGTATGAC	22-037A	CTGTACATGCTACTGATGATGATGACTTTG	
22-038L	22-038L	TGAGAGATTTGGGACCTTTTAAACA	22-038R	CTTCCGCAAAATTCATCTCTCT	22-038E	TTTAACTTTTCTTCAAAATGTTTCTCTCTC	22-038A	GGGCACTGTTTCTTGTAGAAATTTCTTAA	
22-039L	22-039L	TTTGGAACTGTCCCAAGCG	22-039R	GGCAAAATATTTTCCATGAAT	22-039E	CACATATAGTCCAAATGTTTCTCTCTCTC	22-039A	GAGGAGAAACCAATTTTGAAGCTATGATG	
22-040L	22-040L	CAGCCCTGACTGCAACTCTC	22-040R	CCCAAGGCAACTCGGGTTA	22-040E	ATGCTCAAAAGCTCTGTAGGGGCTTCC	22-040A	GGAGGCCCTAAAGACGCTGTTGTGAGCAT	
22-041L	22-041L	AGGCTTTGGCACCTTGAATATAG	22-041R	GGTCCCAATGCTTGGGCAAGT	22-041E	GAAACTGAAAGGCTACAAATTAAGAGACA	22-041A	AGTGTCTGATCTTTTGGAGGCTGTAGACGGA	
22-042L	22-042L	AGGGCTTTGGCACCTTGAAGGAG	22-042R	GGTCCCAATGCTTGGGCAAGT	22-042E	TCTGAGCACTGCTCTCTCAAGGCAAT	22-042A	AAATGCTGTGATGAGGCAAGGCTGTAGACGGA	
22-043L	22-043L	GGGCGGAGGAGGCAATGCTC	22-043R	GGTCCCAATGCTTGGGCAAGT	22-043E	GTCCAGATGTCGCAAGATCCAGACAT	22-043A	CAGTGGCTTCCAGCTCTCCAGGCTC	
22-044L	22-044L	TCTGAGGCAAGGCAATGCTC	22-044R	ACTGGAAGCTCTGAGCCGCTCAATG	22-044E	TTCGAGCAAGGCTGCTCTCTCAAGGCAAT	22-044A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-045L	22-045L	TCTGAGGCAAGGCAATGCTC	22-045R	GAAACAGATCTCCAGCAGCTCTT	22-045E	GGCTGTGAGGCTCTGCAAGGCAAT	22-045A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-046L	22-046L	TTTAAATCTCTACATTTTGGGTTA	22-046R	CTTCAAGGAATATTTCCGCTCA	22-046E	TTCGAGCAAGGCTGCTCTCTCAAGGCAAT	22-046A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-047L	22-047L	AGGTGTGCACTGTCACTCTCAAGCG	22-047R	AGAGCTGTTTACCAAGCAAGCG	22-047E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-047A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-048L	22-048L	TGGAAGCAGACAGTCCAGTGA	22-048R	AGAGCCAGAAATTTGCCACAC	22-048E	GTCCAGATGTCGCAAGATCCAGACAT	22-048A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-049L	22-049L	AGGTGTGCACTGTCACTCTCAAGCG	22-049R	AGAGCTGTTTACCAAGCAAGCG	22-049E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-049A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-050L	22-050L	AGGTGTGCACTGTCACTCTCAAGCG	22-050R	AGAGCTGTTTACCAAGCAAGCG	22-050E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-050A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-051L	22-051L	AGGTGTGCACTGTCACTCTCAAGCG	22-051R	AGAGCTGTTTACCAAGCAAGCG	22-051E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-051A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-052L	22-052L	AGGTGTGCACTGTCACTCTCAAGCG	22-052R	AGAGCTGTTTACCAAGCAAGCG	22-052E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-052A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-053L	22-053L	AGGTGTGCACTGTCACTCTCAAGCG	22-053R	AGAGCTGTTTACCAAGCAAGCG	22-053E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-053A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-054L	22-054L	AGGTGTGCACTGTCACTCTCAAGCG	22-054R	AGAGCTGTTTACCAAGCAAGCG	22-054E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-054A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-055L	22-055L	AGGTGTGCACTGTCACTCTCAAGCG	22-055R	AGAGCTGTTTACCAAGCAAGCG	22-055E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-055A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-056L	22-056L	AGGTGTGCACTGTCACTCTCAAGCG	22-056R	AGAGCTGTTTACCAAGCAAGCG	22-056E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-056A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-057L	22-057L	AGGTGTGCACTGTCACTCTCAAGCG	22-057R	AGAGCTGTTTACCAAGCAAGCG	22-057E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-057A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-058L	22-058L	AGGTGTGCACTGTCACTCTCAAGCG	22-058R	AGAGCTGTTTACCAAGCAAGCG	22-058E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-058A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-059L	22-059L	AGGTGTGCACTGTCACTCTCAAGCG	22-059R	AGAGCTGTTTACCAAGCAAGCG	22-059E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-059A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-060L	22-060L	AGGTGTGCACTGTCACTCTCAAGCG	22-060R	AGAGCTGTTTACCAAGCAAGCG	22-060E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-060A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-061L	22-061L	AGGTGTGCACTGTCACTCTCAAGCG	22-061R	AGAGCTGTTTACCAAGCAAGCG	22-061E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-061A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-062L	22-062L	AGGTGTGCACTGTCACTCTCAAGCG	22-062R	AGAGCTGTTTACCAAGCAAGCG	22-062E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-062A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-063L	22-063L	AGGTGTGCACTGTCACTCTCAAGCG	22-063R	AGAGCTGTTTACCAAGCAAGCG	22-063E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-063A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-064L	22-064L	AGGTGTGCACTGTCACTCTCAAGCG	22-064R	AGAGCTGTTTACCAAGCAAGCG	22-064E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-064A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-065L	22-065L	AGGTGTGCACTGTCACTCTCAAGCG	22-065R	AGAGCTGTTTACCAAGCAAGCG	22-065E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-065A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-066L	22-066L	AGGTGTGCACTGTCACTCTCAAGCG	22-066R	AGAGCTGTTTACCAAGCAAGCG	22-066E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-066A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-067L	22-067L	AGGTGTGCACTGTCACTCTCAAGCG	22-067R	AGAGCTGTTTACCAAGCAAGCG	22-067E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-067A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-068L	22-068L	AGGTGTGCACTGTCACTCTCAAGCG	22-068R	AGAGCTGTTTACCAAGCAAGCG	22-068E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-068A	CAATGTTTATTTGGAAGGCTGTAGACGGA	
22-069L	22-069L	AGGTGTGCACTGTCACTCTCAAGCG	22-069R	AGAGCTGTTTACCAAGCAAGCG	22-069E	TGCAAGCAAGGCTGCTCTCTCAAGGCAAT	22-069A	CAATGTTTATTTGGAAGGCTGTAGACGGA	



Table III 627 single nucleotide polymorphism (SNP) markers

Note: In each block: First part of the first line, Name of the SNP; Second part of first line sequences length shown; G/A or alike, polymorphic site showing nucleotide sequences variation; Other parts, nucleotide sequences flanking the polymorphic site.

01T002      132bp  
CACGTGTGAG GCCTTGGTCC CCACCTGTGG ACTCAGGGTC TCTTTCAC  
G/A  
GACTGCGGGG AAGGCAGTGG GAGCAGCAGG AATGGATGGT GAAAGGACAC AGTGCCCGCC  
CCCCGAGTGT CCGAGGGTAG AGC

01T003      145bp  
CTATAGCCCC TCTGAATGGT CTGTGACACA TGCATGCTTT CAGCTATTCT CTCTATAGCC  
CTTCTGAAC  
A/G  
GTCTGTGACA CCATTATGCT TTCAGCTACA GTTTGCTTTC TCTGGTTTTT CAGTGGTGCT  
CTGGGGAAGG CAGAA

01T006      141bp  
AAAGAAGAGA GGTTTTTGGG GATATTTTTA ACACATCTAT AATCTTTCAT TAACAGCTAG  
AAATTTAGAT TGC  
C/T  
GTACATAAGT GATAGACAAT GAAACAGAGA AGGCATTTCT GAGAGTCTCT CGGCTGTCAG  
CATTGTG

01T008      147bp  
ACTAAGGAGG CATCAACAAC TCTCCAGCA GCTGATGGAG GATGGAACC ACACAAGTGC  
GGAGATTTC A GGTGGGGACT TGGTGGGGGT CGTGTGAGCC  
C/T  
AGGGAGAGAG GACGGAAATT CAGCAAGGAC GTAGAAGAGA GTGCTT

01T009      130  
GTACGGTGCT ACAGGACCCA ACAGAGCCAG AGACTTGACC CAGGTC  
A/G  
TTTAGCCACC CAGCCCCAAG CCAGCAGGGC CAGCCAATGG GAGCCTGTGT CCCACCTCTC  
GCCCCACTC AGACTGTGCT CCC

01T012      138bp  
CAACTTGAAG TAGTAGGTAT TGGAAC TAAG AATGATATAA ATAGAAATTA ACAATTC  
G/A  
GAGATTAGAA TAAGGTGCAG GAAATTACTC TGCAGTGTA TTTTGT TTTT CTCTTAATTC  
AAGAGAGCTT GGAATGCTA

01T013      131bp  
GAAATTCTAT CTCACCACCG TGAAACTCTT CAGTTTTCTA ATTGCTTTAT CAGCAGGGGG  
TATAAAAGGT  
C/T  
ATGAAAGCAA TTTCCACATG CTGTGGCTCC AGGTCTCTGG GTGTGAAGCA GAGCAAGCCT

01T014      140bp  
ACAGCCTGTC ACAGAAGTCC TCTTTGGACC AGATAGGGCT GCCTCACAGG GGTTCAGTT  
TGTCAATTTCA  
A/G

TTCAACAAGT CCTGAACACT TACTCTGTGC CAGGAATTTT GCTGGGCATT AGGGATCCAG  
AGAAGAAGA

01T019 139bp  
ACTGGCCACC TCTGCAGAAG CTAATTGTCC AGAGGAGGGA AAATACAAGT TTATAAATAA  
CTAAAATATC AGGTCAAGCA CATTGCAGG  
A/G  
AGCAAAAGTG GAATAGAATA ATGGGGCTGG GAGCTCCAGG AGGAAGAAC

01T020 147bp  
AACACCTTGC CTGGCATATA GTAGATACTC AATAAAATCT CTGTTGGATG ACTGAGTTTA  
GGCTGAGGGA GAGGGAGAAG AGGGAGGCAG GGAA  
G/A  
CAGGAATGTC TGGGTCCTTC TTAGGCTCTC ATTTGAGTGT CCTCATCCAT TC

01T023 131bp  
AGATTTTCTT GACCGTCTTC TTATTCAGAA TTCATCTTAA ATAAATGTCA CCTCCTCAGA AT  
A/G  
GTCCTCCTTG ATTGCACTGG CCAAAGCGGC CACTCTGCTC CCCAAGTCAC CGTTGAATCT  
ATCCTTTT

01T025 138bp  
AAGGGATAAA CCTCACTGAC TTGGAGGAAA TCAAGAGGAG TGAGCACAGC ATCAGAAAGC  
CCCTTGCCCC CAGACTGCAC CC  
G/A  
CTTTCCTGGC CCTACCTTGA AATCCATCAG GTCTGCGTTG GACACGGCAT TGTAC

01T028 146bp  
CCCAGCGGGA AGCTGTTGAA ATAGTTCAGG GGAGACGGGA GAGGTTCTGG ACCAGGGCAG  
GGCAAGGGCA GAGGGGAGGG TT  
C/T  
AGGACCTGGA GCTCAGGTGG TGCTGATGGA GCAGAGAAGG GAGACAGACC CGCATGTGCT  
TTC

01T029 108bp  
AATTTAGGCC TTTATGTAAA TTCAGAATGA TACAGATTTA GACTTTATAT AAATTGCCA  
A/G  
TAAGTGGCAG AGTCAGGTCT TGAACCCAGC TGCTCTGAAT TTAAAAGCCT TTGCCCTC

01T032 101bp  
CAAAAGACCT CCAAGTCTTA AAAAAAAGA CCTCAAAGGC CTAAATCTGT TCAAAGCTTC  
A/G  
AGGTATTCGG CAAGGATCTC CTAAACTCTT TTTTGTCTT GGTGGTATGA

01T035 Rsa1  
GTGCTCATGA GCCGCACGGG-GCCAGCGCTG GTCCTGGGAC GGGT  
A/G  
CGGCCACCGG GGGCGCTGCT CAGCGTGCCC GTGCTCAGCA GCCT

01T037 122bp  
CCATCAGGTA ACTGACAAAC TCTAAGGAAG CATCTCTGTT TTTCTGGCCC TGTACTAGGT  
TCTGGAAGG  
C/T  
GGTGAGCCAG CAGGCAGGCC TGGGACTGGG AAGCCAGCAC TAGGGCTCAG GG

01T038 130bp  
TCTTAGCAGG GGGACAGCC TAGGCAAAGG CCTAGAGGCT GGAA

Table III

A/G

GGGGTAGGTT TGTATGAGCC ATGGTGAACC AAAGTGTGAG AAAGAAATGG CAGGAGAGGT  
 TTGAGTCCGT TAAGAGAAGC CTTGA

01T039 130bp

CTCTCTAGTA AACCCGATCA CCTCCCACTG GCATGTGCCT AACACGTAGG AAGTTCTCAC  
 A/G

ATGCCCTATT GTTAATGATG GATGACTCTA ACTATGATAG CTAATATTTA TTGAAGGCTC  
 TGAGAAGCC

01T041 149bp

TCTCCAGTGA GTCTGGGGGC TGGCAGGGTG ATAACACGAG GCCAAGGCTC AGAGAACTGG  
 GCCCTGGTTC CTAGGCCTGG CT

C/T

TGACATTAAA AGCAGTATGA TCTTTGTTTG ACAAGTTATT TCACTTCTCC AGTCTTCAGT  
 TTCCAC

01T042 127bp

CTCACTCCCT CAGGCCTCCG CCCAGTGCTC TTTCCACAG AGGC

C/T

TACCTGACC ACTTGATCCC AAACAGCCCC TGCCTGTCCT CCCTTCTCCC TCCCATCCAT  
 CTGTTCTGC ATCATCTTCC TT

01T043 113bp

ATTCTCGAAC TTTCACGCAC AGAAGAATCA CCCAGAGGGC TTGTGAAAAC ACAGA

T/C

TGCTGGGCCC CAGGCCCAGA GCTTCTGATC AGTAGGTCTG GCCTAGGGCC TGAGAAT

01T046

TCTGAACACC CGGTTTATAG TCCCAGTCCT GCCACTGTAG GACATTGAAT AGGTGATGTT  
 ACTCATCTGA AATTGTATCT

A/G

TTTTGATAAC ATGGGGATAA TATCTCTTCT CTCTACTTGA ACAATGAGGT AACACTGATG  
 ACC

01T047 147bp

CAGAGGGGTT GCCGTTGCTC CTTATCCTCC CATCATTTGA TAATGTCAGT TTTTTTTTAA  
 ATTTTAAACCA TTCTAATAGG CATGTGGTAG TATCTCACTG

C/T

GGTTTTTCATT CATGTTTTTC TAATAACTAA AGATGTCGAG TGCCTT

01T048 140bp

CCACACCCTA GAAGGCTGTA GAACATGAGG ACATGAGCCA TGTAGGACGT GAGGATGA

T/C

GCCAGGGTTC CAGTGCAAGC TGAGACTTAA GGGTACCTTC CAAGAAACCA GGAGGAAAGA  
 GCGCAAGGAA CTGGAGTTTT T

01T051 130bp

CTACCCTGCC TCTGGGCCTT GACCTGTGCC CTCTTCTTCC ACAGCTGTGA TTGTGGGCGG  
 GGTGGTGGG

C/T

GCCCTCTTTG CTGCCTTCTT GGTCACACTG CTCATCTATC GTATGAAGAA AAAGGATGAG

01T054 133bp

TGAGATGGCC CAGACTCCGT GCAAAGGAAG GCAGGATGAG GAGGAAGTGA CC

A/G

TCTTCGTCAA GGTGCACAGA GCTGCACAGC AGCCCAGATG GCTCTGCTGA GAAGACACCT

Table III

CATTTGGAAG TAAACACAGGC

01T055 118bp  
CCTGGGGCCG GTGACAGGAA AACTAGACCT GAAAGTGTGA GAGGAAAGAG AAGTTGCTTG  
AACTCAGAGA G  
A/G  
CCTCTGTGGA GAGGGCCATC CTGCAGGAGC TGAGATCTTC CACTAA

01T056 122bp  
CACAAATGGGA ACAATAAATC CAACCAGAAG GAGGGCCATG TGTGTGAGCT TGACAGTGCA  
A  
T/C  
GCATGGGAAA AGGAAGAGGG CGGGTCTTCC TGGGTTACCA ATTCACATCC ACCACCATTC

01T057 137bp  
CCCATTAGCC AATGAACAGC TTGTTTCTCT TCCTGAAAAA AGGATAGATC TTACA  
C/T  
TCCCAAAGAA TCAGAGCCAG ATAACAGCAA CAACTTATT GATCAGTTAC TATATGGTAG  
CCATAGTTTT GTGGGTTTTT T

01T058 142bp  
GTGTTCCCGG TCGGCATATG ATGAAAAACA TGGGTTTGTT CCTGGGCTAG GTCTCGGTCC  
GAAGCATGAA GGGATTA  
C/T  
TAAACCCCTC CCAATTACTA TAAAATAAGA CAGTAATGGT TTAGATTATC CTTTTTAGTG  
GTGG

01T060 130bp  
GGACTGCTAC TACACAATGG AGGTAAGGAA GATTATGTCT GGAATAAAGA AGATCC  
C/T  
TTAGGTTATC TCTTAGTATT ATCATGGCCT ATGATTAAGA TCAATGAAAA ACCAGAACAA  
CTCAATCCAG GCA

01T061 125bp  
CCAGCGTTCT GCAAGGGGCT GGGTAGAAGG GGCTGGCATG GGCATCTGGA ATCCTTCAGC  
CTAGTCCTCT GGC  
T/C  
CGGTGATGAA AGCCCAACCA CTGTTCTCAG ACCAGCAGGG ATAGTCTATC C

01T062 142bp  
AAATGTGGTA CATGGTCTTT GTAGTGATGC CTGTTTTTCA AAATTTCACT CTACAAACAA  
CCTCACCA  
T/C  
GAACTGTTGT GAGAACTGTG GGAGCTATTG CTATAGTAGC TCTGGTCCTT GCCAATCCCA  
GAAGGTTTTT AGT

01T063 95bp  
ATTCATCACA TAAAATGCAA CTACCCTGTA ACTCACATAT GTAAAT  
C/T  
CAATAGCAAG AACATTCTG AGATTCAGCA GTGGGATTTC AGAAAGCT

01T064 146bp  
GTGGTCCTAC ACAAAGA AAC GAATATTGGA AATGGCATTT AGAAAGCATG TACTACACGT  
TTTCTTATAA TTAAATCTT TCAAAAAATA TTTGACGTAA  
T/C  
AAATAAAAGT AATAATAATG AATCACAAAG GTTATAGTGC ATAAA

Table III

01T065 141bp  
GCCACTCCTG ATGGATGATC TTACTTGCTT TGCCAATGAC AGGAGTGAGA TGACCCATTT  
CTAGCAAAGC CATGAGGCCG TATCTG  
T/C  
TGGAGCTTCC AGGGGAAGAC TTCCTTGCTT TAGAAGGACA CAGAAAAATC TGTC

01T066 148bp  
TTGAAAGTTC TGGTGTATAG CCCAAAGGGG ACAGACAAGA AACTTAAGAG TCTG  
A/G  
AAGGGGTAAC AGGGGCTTAC GTACTTCTGT TTCTTTGATC CTTTATGAGT TTTCTCTGTT  
TTTTCAAGCTG ACCTTTCCCT TGAGTGACTG GAG

01T067 143bp  
AGAGGGATAC TTGTAAACTG AAAAGGCTGA GCCCAGAAGA TAATACACCA ACCAACCTCT  
TTCTTA  
C/T  
CATTCTAGG CCCCAGTGTT ATCTGACTAT TCACCTAAAA TTGTAGAGAC TCGAAGGGTT  
GTGGCAAGAA CACTGG

01T068 125bp  
TACAATGCTT TTCTTCAACA ATAAACAGCA AGATCAACAC ATGTACT  
A/G  
GTATAGCTGC TTAGCATTTT TAAGGGAAGA ATAAATTATA TGGCCAGCCA GCTAGCAAAA  
TAGAGTGAGC TACCACA

01T069 131bp  
TATCCCTCCT GCCATCCGTG GAAAAATTGT CTTCCACGAA ACTGATCCCT GGTGCCA  
G/A  
AAAGGTTGGG GACCACTGTC TTAAAGCATG CCCATAAGGG TGGGTAGCTC ACTGGACATC  
TACTGAACAA TTT

01T070 131bp  
TTGTCTCCTC AGGTAGTGAT GAATTAGTTG CTGTCACAAA AGGAGGGAAG TAGCACCCAA ATTAA  
A/G  
TTGCTTAAGA GAGGAAATGT ACATCTTGTA TAACTTAGGG AGCGAAGAAA ATGTAGGCGC  
GAAAG

01T071 141bp  
GGCCCCTATT CCAAGAACCA CGCTGGGCCA GGGTACATGG CTCCCTTGGA GCTTTGATGG  
CACTTC  
T/C  
TTGGGAAACA GAAGCTGAAT GTTTAAGAAG CATCTGTCAT TATGGAAACG AAGTTGCCAG  
GCCATTTTTT CTTT

01T072 146bp  
TTGTTTCGTTA TGTATCACTT CTTTAAACC TCAAAGGCAG GTTGATCAGT AACCAGGAAG  
AATGGATCTT TGAATTTCTG AATTCTGG  
T/C  
AGTAAACTT TCCGATGTCA TCCAAATCCC ACCCGAATTT CTTTTTAATT GAAAGA

01T074 102bp  
ATTAGCACGT CAGCTTCTC TTGTGGTATT TATGTGTTTA TATAACA  
T/C  
AGTTCATTGT TCCCAAATGT TAGTCAACTC CAACTATAAA TCAAGCCCCA AATC

01T077 124bp

Table III

CAAGAGAGGT CCCACCAGGA AATATTATAG TCAAACGTG AAAGGCCAAA GGCAAAGAGA  
AAATCTTG

A/G

AAACAGCAAG GAAGAAGCAA CTGTTTACAT ACAAGAGATT CTGAATAAGA TTGTC

01T079 127bp

GATGGGAGCC AAACATCATC CTTTTATCAG GAACCCACTC CTGTGATAAC TAACCTACTC  
TCATGATAAT GACGGCAGG

A/G

CCCTCATGAC CTAATCACCT CTTAAAGGTC CTGACTGTCA ATGCTGT

01T083 129bp

CCTCTTATCT GAGAATGACC CTTCTCCCCC AAGGAGTCCC AAAAGGTGGG CTTCTTTGTT  
GATTTAGAGA

A/G

TCGATAATTC AGTAAAGTCC CAAGTAAATG GCACAACACA AGCTCAGA

01T084 142bp

CAAAGGGACA AATACTGTAT GATTCTACTT ATATGAGGTA CTAGAGTAGT CAAATTCA

C/T

AGAGACAGAA AGTAGAATGG TGGCTGCCAG AGCTGGGGAA TGGGGAAATG AGGAATTAAA  
GTTTAATTGG CAAGGAGTTT CAG

01T087 137bp

GCTTCAGAGC TCTGCCAGCT GCCATTCTAC AGAGGCAAGC CCCTCCGGCC CCATCTGGCC  
TCCCTGACCC AGGG

C/T

GCTGGCCTCT GATTGCATTC CCCTAGTGAC AGGGAGCTCA TTAGGGCCTG GGGCTTTGGG  
GA

01T088 145bp

CAACCCCAAG ACTCCCAGGC ACATGGGATG GATGTCCAGT GCTACCACCC AAGCCCCCTC CTT  
C/T

TTTGTGTGGA ATCTGCAATA GTGGGCTGAC TCCCTCCAGC CCCATGCCGG CCCTACCCGC  
CCTTGAAGTA TAGCCAGCCA A

01T089 146bp

ATTTACATGC ATTTAATCCA CGCAGCAAAA TCCTAGGAAG ACAGTATTAT AGACCCTATT  
TTGCAGTGAG TAGACTGAGA CCTAGAGAGG C

C/T

GAGCCACTTG TTCAAGGGCA TACAACCTACC TGGTGGGGGA ACAGGACTGG AAAC

01T090 147bp

CAGCATGTTA TAAATGCTAT ATGGAGTAAT AAGTATGGTA AGAGAATAAT GATTGAGGGT TGGG  
A/G

TTACAAATTTT AAATTGTGTG GTCAGGAAAAG GTGACATTTG AGCAGAGACT TCAGTGAAGT  
GGGTAAGTGA ACCATGTGGA TC

01T091 147bp

ATTTGGAGCC ATAAAACATA TCTAAACTAA TTAAAAGAA TGGAATTCAT ATAATGTTTA  
CTCTCTGGCC ACAA

C/T

GGAATGAAAC TAAAAATAAG TAACAAAAAG TTACCCAGAA AATCCCCAAA TACTTGCAGA  
TTAAACAACA CA

01T094 112bp

TCGAATCTCG CCCAAAGTGA CGAATAAATC CGGACTCTCA GCAACATGGG CTATAGGGAG GATCC

Table III

C/T

TAAGAATTCC TCAGTGACCA GATAACTCTG TGCATAGACC AAGGTA

01T096 116bp

TCAGTGCCAG AAAGATGTGG CTTAAGTTCC TGCGACTCCC TTAATGTGGA GCTCAGACAC T

T/C

GCCATGGGGA GAGCCAAACT GCCTTCACAG CACTAGATGC TCCATAAGGG ACCA

01T097 148bp

CAGGGTCCCT TTCCGTAGAG CCGCCAAGTT CTGGTTCCTT GTGGGTCCCG C

C/T

ATGCACCTTC CATCCATATG TGCACATACC AATGTGCAGC TCTTTTATT CATGTAGTGG

ATTCGGATCA CACATATAAT ATGCCTGTGA CGACTT

01T098 134bp

GGCCAAGGTA TAATCACACT GGTAGCTGGA AAGCCTTCTG GGCTGGGGTG CCATAGGCTG

T

A/G

TTTGGGTTCC AGTTCAGCG CTGACTTTGC TCTATGATTC TGGACAAGTC ATCGCCCTCT

CTGGGCCTCA GT

01T099 145bp

CCATTGCTGT GTCCAGGGC ATTTGGCAGC ACGGCTGGGT GGTGAC

A/G

AGGCCAGGAG TAGTATGTGC AGGCACAGGG TGGGCGTGGC AGCTGTCACA TGGCAGAGGA

CCCGCAGAAG CTGCTGATGG CTGGAAGGTA ATTAACA

01T102 130bp

AAGAAGCCAG GTACCAAAGA GTACATACTA TGTGAATCCT CTTAACATGG AATTCTAGAG

CAGGCATAAT GGTCATAGTG AC

A/G

TAAAGCAGAC CAGCGGTTGC CTAGGGTGAG GAGTAGGTGA TGGGAGG

01T103 148bp

GACAGGGTGA TCAGGACAGC TTCTATAAGA AGGTGAGGTA TGAATTAATG C

C/T

TAAAGGAGGG GTGAACATGA GCTAGGCCAA TTGCAGGAAG AAAGGGTCAC CAATGAAAAA

GCACAAGCTA GGATACATCC CAGGAAAGAG CCAGAT

01T104 109bp

CTGGGAAGAC GTCTCTTCAA AGCTATTTGA AAGAACTGTG CTTTA

A/G

GAGATAAAAT ACCTAAACAA GCAAATCCTC AATTTCTTTA CACAGACTTT CTGTCATTAG

TGT

01T105 140bp

AAATGTCTGC AGTCTGGCCT CTGTCCCCTT GATGCCAAAC AAAAC

C/T

GCCCTGCCCA AGGTCACTGT TGTAATCTA AATGACACCC CTCAGCAGCA GTGGGAGCAT

TCTGTCCTGG TGTGTTCTCT GACTCTGTGG CCTC

01T108 134bp

GGATGAGAAG GAAACAAGCC TGGTGAAATG GAATGGTCAG AAAAGCCTCT

C/T

TAGCATAGTA CTAATTACGG GGTAAATTC ATGAGGAGCC TGATTTGGAA GTTCAAAGA

GGCGAGAAAC TAGACAGAAT GAA

Table III

01T109 107bp  
 CATTGTGTG CTTGTCTCCC TCAAGAATAG GGACTTCTCA AAAATCAAGC TACATGCTGC  
 AAGTGCTTGT ACC  
 C/T  
 AGAGCTCTGA ATCTGACACA AAGTAAGGTT CATACGCATT CAA

01T111 122bp  
 GGCTTATTTG ATGGAAATGG TAATAATGAT AATAATAACC ATGAACCTAC TGAATATGAA  
 ATATATTAAT AA  
 A/G  
 CCATCTTAAA ATGTTATTTA CTCTTCACAA CAATGAGAAA AATGTGTAT

01T117 144bp  
 GTCTCCATCT CTCTTAAAGG AAAAAAGAC GACATTACAC AGCAACATGA TTATTTAATT  
 AATAGCTTTT CC  
 C/T  
 TTTGATGCCA GTCTTGTTTT AGTTATAATA AACTAATAG GTATATCTGT CAAAGGACTT  
 ACAAATAAAA G

01T118 126bp  
 TGCCAATCTT TCTGGCAAAA TCAAAAATGC TTCCAAACCC AGGGAAGCAG  
 T/C  
 ACTACTCTGT GTGAGAAGTT CTGTATAAGC ATAGCTATCC CTAAATGCAG GCTAGCAACC  
 ATCTCCCATC ATAAA

01T119 143bp  
 GCCAGAGGCT GATGGCAGTG AACAAAACAG ATGAGTTATA GCTTTAC  
 C/T  
 AGTTGGTGAA AAAGAGAGTT TTAAATAAAA AAGTTATACA ACTAGATATA ATTATAAATC  
 ATGTTTACAG AGTTATGTGT GAGAATTAAA AGGGA

01T120 142bp  
 CCTATAATCC CAATGCTTTG GGAGGCAGAG GTGGGAGGAT TGCTTGAGGG CAGGATTTC  
 AGACCAGCCT GGGCAATATA GCAAGACCCC ATTTC  
 C/T  
 ATAAAAAATT TAAAAATTA GCCAAGAGTG GTGGCAGGCT CCTGTA

01T121 120bp  
 GAGGCAGGGT AAGCAGGATT CAGATTGGCG AGTTGGAATA CTTTCAGCAG GCTCAGGGCT  
 GGCTGTCTTT AGTTGTC  
 C/T  
 GGTACCTGGG CCTGGGGTGA TTAGAGGCGG GGAATACTGG CC

01T127 140bp  
 GGAGCTGCCC AGAAACAGCC TTGTGGGGTG GGGTTGGTGT CTGACCT  
 T/C  
 CCTCCCCGGG GGCCTTCGCA GGCTTCTCTG CTGGTGCTTC TGTGCCTGTG GGTCTGGATT  
 CCTCCAGGGC CTGATCCTGG GTGCAGATGC AG

01T128 142bp  
 TCCCAGGGGC TTCTGTGGCC TGCTGAGGCG CAGTGGGGGA GGCTGGCAGA GGCAAGAGGG  
 CAGGGCCTGA GGGATGG  
 A/G  
 GATGGGAGGC TCTGCCTCTC ACATGTCCTG TCCTCTCCAG ACCCCAGGGC TCCGTCCTCT  
 GGAC

01T129 141bp

Table III



ACCCAATATG CCAGTTAATA CTGACATTTT CAGTGGGAAG GGAAGAGGTG AGAAGATAAC  
ACCTGAGTGG GCTGATGAGC C

A/G

GAACAGTTTA AGTGGGGGAA AGGTCTGGCA TTGCCTTAGA GCTGGTGACC AGACTCCCC

01T131 133bp

CCTGTTATTT TCCAGAATAA TCAGTGATAC TCTGTGATAT TGATAATCTA CTTGTTGGC  
CCTTACCAA

A/G

TTACTGGGTG TGAGTAACAG CTGACTGTAG CTCCCTTTCT CTACCCTAGT GCTCTGGAAG  
GAG

01T133 126bp

AATCTACCAA TCTGACAAAG GGCTAACATC CAGAATCTAC AAAGAACTTA AACAAATTTA  
CAAGAAAAAA ACAACAA

T/C

CCCATCAAAA AGTGGGCAAA CAATATGAAC AGACACTTCT CAAAAGA

01T135 129bp

TTAAAGTCTT TTATGCCTTC CCACCCATCA TTAAAAATTA ATAAATTTTG TCACTCAGCC  
ATTTACAAAA TAATCTGATA

C/T

TACAGATTAT TTTATTTTCT TCTACAAGAA AACCATATCC TATTTCT

01T137 148bp

AAAAAGGAAA CCACCTTCT ACCAGGGACC CTTAGATCGA .CCCCAGGAGG AGCCCTAGAT  
GCTGTTCCC

A/G

TACCAGCCCC TCTCCAGCGG GAAGTAGCCA GAAGAAGTTG TTGCCCAATT CCCCCTAACA  
GCAGTTAGGG ATTCCATT

01T138 105bp

GAAATGATTC ACACCAATTC ATGATAGAAG GTTGCACTTG C

A/G

GAGGGTTGGT GTATTAGTCC ATTCTCACAC TGCTACAAAG ATACTACCTG AGACTGGGTA ATT

01T145 149bp

GGCAGCTGGA GGTAAAGCAT CTAAGATTAA TTCCTGAACA CCAACATAGA AAGGCCAC

C/T

AAGGGAGTTG CTGCCTGTCT GATCAGGAAG CTTCTGGAGT CAGGAGCTGC TTCTTTAGTT  
CCTGGTTCCA GGATCATCCC AGCTCTGCTG

01T146 127bp

ATGTGTTAGC TCCCACCTGT AAGTGAGAAC ATGTGGTATT TGATTTTCTG CTCCTACATT  
AATTTGCTTA GGATTATG

A/G

TCTCCAGCTA CGTCCATGTT GCTGCGAAGG ACATGATTCA TTCTTTCT

01T147 140bp

AATATGATGA AGCGTAGTGA AACACATAT GTAAAATGTT ATTTACA

A/G

TGGCAAGTAC TTGAGATACA TTCAGTAATG AAGGCTATCA TCATTGTTAA TGGCAGGAAT  
TTTCAAGTGA GTCATTATGT TTACATGCCA CA

01T148 102bp

AGGAAGGAAT AATAGAGAAA CTTACCCAC TTCTTTGATA AGTAGGACC

G/A

Table III

GACTCCATGA GCCATTGATT ACTTCTTGTG TCAGACTGGC ACATATCAAG GA

01T150 100bp  
TCAGAAGAAT CGTTTGAACC CTGGAGGCAG AGGTTGCAGT GAGCCGAGAC AGC  
A/G  
CCATTACACT CTGGCCTGGG CAACAGAGAG AGACTGACTC AATAAA

01T151 126bp  
GTACATTGGC CCCTTTTATC CATAGCTGGA GTGGCTGGGA CACAGGACAC CAA  
G/A  
TCCCTAGGCT GCACACAACA CAGGGACTGT GGGCCCAGCT GATGAAATCA GTTTCCTCCT  
GGGCCTCTGG GC

01T152 134bp  
TTCTTCTAAC TTCATACTGG CTTGTTTGTG AAAGAAAAGT CTTTGAAAAG GCTACCTG  
C/T  
AGGTGATAAA GATTTTTTAAA GTATTCTTTT CTTCTTTTTT ATTAGAGAAA ATCCAAAGGG  
AGTTTTAAAA TTTGT

01T153 141bp  
ACTGGATTAT GCTCCAGGTA TCTGACAGGT TTTCAATACT ACTA  
A/G  
TATGTTTATT ATAGCATAAA AGGGCAATAT AAAAATAATT AAGAACATCA ACTTTATAAT  
AAACAAGACT AGATATTGAA TCCTTGCTCTG CACTTC

01T154 117bp  
CCATTCTTCC CGTTAAATA GCAAAATCAA GGATACTAGA ATAATGTATA ATGTGTTCAA  
CACTAAATCG  
C/T  
ACCTTCGAAT TTATATACAG TTTTAAAGAC ACTGACCCTA AGGAGA

01T155 149bp  
GGATAACCTG ATGAAATTCA AACTTCTCTG AGTATCCATT TCCTTATCTG CTTATTCAA  
C/T  
TGACTAGTCA CCTCCTCTCT TTGGATATCT AATAGGTACT TAACATTTAA AATGCCCCAA  
ATTGAGCTCC AGATTATCAC CATTCCCCCT

01T156 130bp  
TCCTTCTCCC CTGGTGTTGG GGCTTCTATT GTGAGGTGAC CTCTGGCTG CTCCCTTATG  
GGTCCCAGGA CCTAACCACA GTTG  
A/G  
CCAATCATAA TCCATCAGGC CCAGTTTGTT CAAAATGAAT TGCTC

01T157 135bp  
AGCATGTTTCG GATTTTCATGA CTCTTGTTGGT TTTGTTTCCTA GACAGGACCT ACCAGGGGAG  
CCTCCTGCAA ATGAG  
G/A  
TGGTCTTCCT TTTCTACTCA TCACATTCTA TGCCTGCCCT CTCTAACCTA CATGGTATA

01T159 139bp  
GTTGAGTCAT TTGGCCTCCT TGATCCTCAC GTAAATTGTG GCATTATTAA AGTT  
C/T  
GGTCTACATC AAATGGTCAT TACAAAAATT CAGTAAGTGT ATAAATATAC TTTTAAACT  
AAAAAGCTCT CAGGAGGCTG AAGT

01T160 147bp  
CCCCTATGTC CCACAAACCT GCCAATCTCA GATTTCCTGTAT CTCAGTTAA GATTCCTTCA G  
A/G

Table III

TTTTTAGTTA TTCAGGTTAA ATAATCTTTG ATCTGTATCC TCTATTAAGT CCATCAGAAA  
ATCCTGTTGG CCTTTCAAAA TATAT

01T162 136bp  
AATTAGGTTT GAAAAGGGAA ATAGTAGAAT TAGAGTTGGG TTTAGAAACA AAATTAGTCT  
TGTAATAGTA ACTATGCT  
C/T  
TTCTAGAGTG AGGCAGTATA GTCATGGAGG AGAACTGCCA AGGGATTATT TTAATGA

01T164 122bp  
TTAACTTGTT CACGTTAAGT CCATTCATAT ATTTTGAATA AGGTATAGAG GAGAGTTTTT  
GAGTGA CTCC TCACTC  
G/A  
TCTGAAGGTC TGTGACCTAT GAACTGCCTC AAGGCTTTCT CTTCA

01T166 138bp  
CACATTTCTT TTCCATGTGG TATGTGGTGA AAAACAGAGA AACAATAAAA CCCAAGAAGT  
CTTATTATTA TGACTCCCTT CTTAAAATGC C  
C/T  
AAAGAGCTCA AGAATAGTAT CTTGGGAAAA TTACTATGTG TATGGA

01T167 105bp  
ACAAAATTTT AATGCTCTGT GGATCATTAT CTGGCAACAG ACCAACAGCA GA  
G/A  
CATAAAACAT TAACAACATA AAGCGGGTTC TGAGTCCTTG GAGTTTCTAA TT

01T169 131bp  
CATACAACCT CCCAAGACTA AACCAGGAAG ATCAAATTCC TTACTAGACC AATAACA  
T/C  
GTTCTGAAAC TGAGACAGTA ATTAACAGCC TACCAACCAG AAAAGTCCAG GACCAGATGG  
ATTTACAGTC AAA

01T171 133bp  
GCAAAGGGTA AGAAGAGGAA GTGGCTTCCC TTAAGTTAGA AGCTGTTTTT ACCTATGGGC TG  
T/C  
GACAATGCAC TGGCCATGTG TTCTAGACCT AATCTGGGTG AGTGAATAAC TGGGAGGATG  
TGGAACCCAG

01T172 148bp  
ACACTCCAGG CCTGATACTT CTGGTGTTAA GCAATTTGCA AAATGATATA CTAATGACCT  
TTCAAAAAGT TATT  
A/G  
CCACATCTGC TCTTTGTCAA GTGCAAGAGC CTAGTATATA GAAAATAATA TTAAGCTCCA  
AGTGAATACA AGA

01T173 148bp  
TTATAGAAGA TCCCCATTGA CGATGCTTTC AAGTTGAAAG AACATTTAGA TAAGCCATTT  
GATATAGAAG TGACTTTTAT TTCACGGTCA AAACAATT  
G/A  
TCAGCCAAAG AAAGTTCCTA ATTTTGTGTA TTTGTGCACC ACAGTAAAT

01T174 140bp  
AGACAGTTCA CTGTATTCCT CCCCCAATTC CTAGAAGAGT AGTAAGGGTC TTAAGGCGGG  
AGAATGAGAC CTCCTGAAAT  
A/G  
CTTATGAAGC CTTCCCTTAT CAAGTACTCA CAGCCAAATA TTTCAGAGTG GCGTTAATT

Table III

01T176 147bp  
 CAGCTGAGGC ATTAATATTC ATTGGATTGG GGGGGTGGTT CCAAGATGGC  
 T/C  
 GAATAGGAAC AGCTCCAGTC TACAGCTCCC AGTGTGAGCG ACGCAGAAGA TGGATGATTT  
 CTGCATTTCC AACTGAGGTA CTGGGTTTCT CTCACT

01T178 134bp  
 CCTGTTAATA GCCACTACCT TCTTTTCACA TATCACACTT CCGCTTGCTT GTTAACATTC  
 CTCAGTTTTT ATTTATGG  
 C/T  
 TCAATGAGTC TGTTTTGCTT TACTTTATTT TAATTACTAT AGAATGTACT GGTAACTTTC TGATG

01T180 119bp  
 TACCAGATTT GAGGCTCAAT ATCTACTTCT GAAGCTGGGA GTTGCAATCC  
 C/T  
 TGAGTTTACC ATTTTCTTTC ATCACTTTGT CCAGTGAAC TAGGACCAAC CAACCAACTT  
 TGTTATGT

01T182 139bp  
 CATGCCTTTG TCAGGAGGCA TTCCCTACGT TCAAGTCTTA AGCATGTGTC CTGTATAAAA  
 TCAGTCTTTA GCGTCTCCCA AAAGAGCTAT CACTT  
 CCT  
 C/T  
 CTTTTATGAA CTTGCTGTAT CTTGTCTCTT CACTTGAGCA CCT

01T184 129bp  
 ACCCAGCCTA GGGCATGGCA CGAAGGAAGC ACTCATGGGG CTTGGC  
 A/G  
 CATAGTGGGA GCTTGCCCAG TGCAGGGCCT GGCTCTTGCG TGCTCAGGAA ATGTTTGCTG  
 AATGGAATTT CAGTGAATG GA

01T185 134bp  
 TTCAAATTGT AGATCTCCCC CTCCTATCTT CCACCCATA GCTAAGAAAG GAAACCCAGG  
 GATAGAACTA ATTGAACTCT ATTAGCCAG  
 A/G  
 GGCAATCGAA CCCAGTGCCA ATAGAGAGAT GGAATCCCAA TTAG

01t187 145bp  
 GCTGCAATGG CGTGCTGTGC TTGGGGGCAT GAAGTGTGCA GGGGTAGGTA TGCTGGCCCT  
 GAGACTTTCC CCCGTGAGAA TTTCATTGCC ACAGC  
 A/G  
 CCAGTGGGTG GATCGATAGC TTTAGGAAGG TGAGGTTTCT TTTGTGGAG

01T188 143bp  
 TAAAGCTGTA ACAGTTAACC TCTTCCACAT GCAGCATCTG CAGGCTGCTT CCCTTGCAGA  
 CAGTTTACAG TCTCTCTGTG  
 A/G  
 TAGTGCCAAA CTCTATGACC CAGGCCAAGA GTACAGTGAA TTTGTCAAGG CCACAAATTC  
 AA

01T189 140bp  
 CCAAGATCGT GCCATTGCAC TCCCGCCTGG GCGACAAAGT GAGACCCCAT CTCAAAATAA  
 GTAAATAAAT AAACA  
 G/A  
 AAAAGAATTT CTTAGACGAA ACCTTGTGCC TTTTGTGCTC AGTTGGATAG GAAGTGAGCA  
 TCTG

Table III

01T192 148bp  
 AAACATTTTT AGAGGCCAAG TGTTTCATGTT CATTCTTTAT CCACTACAAT CATATACATC  
 AACTTTGAAT GGAGTTGTTT GTGATTTGGC CTCATTA  
 A/G  
 GCTAAAATGC TTATGAAGAT AGATCTGCGG TTTGAGTAGC TTCAAATTTA

01T194 135bp  
 AAGACTTCTG AAGCACCAGT ATCTGAAGAG AAAGCAATGG AACACTGAGG AGAGATA  
 C/T  
 GAAGAAAGTG GGACCATAGA GGCAGAGAAA ACCATGAATG ACTATGCTTA TACAAGCCAA  
 ATGCAACATT TCAAGAA

01T195 132bp  
 GTAAAGGGAG TGGCCTGTTC AATATGGGAA AAGACTTGCC ACACATTAAA GCATTTTTTC  
 A/G  
 TCTTATAAAA TTGATGTATT CTTGGAAAGT GTGTAAATTC ATTTTACATG AAGGGAATAA  
 TTTTCATGTAA AG

01T196 142bp  
 TGCAAAATCT TGTATTGCTT GACTACCCAA GTATTAACTG AAATAGTCAT GCCCATCAGA  
 CACAGGCAGA GTTTATATAG TGAAACAACT T  
 A/G  
 AAACAGAGTT TATTAACAGC AAATATTCCT ACACTCCATA GCACAGGAGT

01T198 116bp  
 TGGCATTATG TGCCTCTTGA TGTGATGCAC TAAAAAGGAT ACATCATAGA GTATTAAGGC  
 CAAATATGCA  
 C/T  
 AGATGAATTT AATCAGGAGA AAGCAATCAC ATAAATTGAG GAAAT

01T200 138bp  
 TTTACATGAT GATGACACAA ACACTGTAAA GGACCTCTGG GTTACTTGTT TATAAGCTAG  
 TATTTCTGA ATCAATTT  
 C/T  
 TCTGATCCCT AGATATTTGG TAGGTGAAGT CATACCTATA TATCCCCACA CCCTAGAAC

01T202 139bp  
 CCTTTTCATT TGTCATTGTC TATCACTACA CTGTAAGTAC CACAACAGAT GGAAACTTCT  
 CTGTTTGTGTT ATTAGT  
 A/G  
 TATCCTCACA ATATTTGTGA AATGAGTGAG AGACTCAGGA TACAAAGGTG GAATAAAGC  
 AG

01T205 107bp  
 AGTGGCTTTC AAGATTCTCT TTTTGTCTTT GGATTTCAAC AGTTTAATT  
 C/T  
 TGATGTGTAT AGGTGTTAAT CTCTTTTGAG TTTATTACTA ATTGCAGTCT ATCTGGC

01T206 121bp  
 AGATGCTGAC CACAAGCCTA AAACATATGAC CCATGCTTCT GGTAAACAG CTAAAAATTG  
 GGGTTCCC  
 A/G  
 TGGCCCCTTC CTCAGTTTTG ATTAATTTGC AAGAGTGGCT CAACAGAGCT CA

01T207 124bp  
 TGGCTTATTT TTTTGCATAA CAAATTAGAA AGCAATTCAT AAACACAAA AGATCTGAGA  
 AGATCTGTAA TTTCTA  
 A/G

AGATTAATAT AGTCCGTGTG ATCAGAGGAA TGTCATTGCT CAGCAGT

01T208 120bp  
AATCGGAGAG CAGATTCTAG TAGTTTAGCA GAAAGCAAAA TAGAACAGTT AATAATCATT  
AACTTAGACT GC  
C/T  
GAAGGCACCT GAACTTAGAG TAAAGCATGA AGTGCTTGTC TTTGCCA

01T209 127bp  
AAGATAATAG CATGATGCTG CTATAAATAA ATGTATAGAT TGATATCTTA AGTGTTCTGG  
TGCTGAGTTA CTCA  
A/G  
AGAGAAACAG ATCTCTAAGT TTCTGGTGAT GAGTCACCAC GTGAGAGAAA TT

01T211 100bp  
GTTAAAATGA GCTCAAGATG TGTAGACGTA TTATGTTTTT TTAGGCTA  
C/T  
TGTTTTTTTTG CAACATTTAG CAAATGAATA GGATAGTACA GGGCTTTTTT A

01T213 137bp  
ACGCCAGAGG CATGGAACAT TTTCTCCATC ACAGCTCTCA AAAGGAGTCA ACCCTACAGA  
CACGTCAATC TCAGACATCC AGC  
C/T  
TCTAGAACTG TGAGACAATA CATTTCTGCT GTTTAAGCCG TCAAGTCTGT GGC

01T217 134bp  
TTAATGAGAA AATGACCCAA TGATAATGTA TATGTAATTA AGATTTTCATT TGCTTCCCTA  
TACACC  
A/G  
TGAGAGTTAA TAAATATAAT CCTCTATGGG CAATTTCTTT AAATCACAAG AATATTGGTC  
CCTGAGG

01T220 126bp  
AATTTTCTTC ATAACACTGT TCTTCATTAA AAGGTAGCTT TATTTTATAT CTCAGTGATA  
AAAAGCCACC AAATCA  
A/G  
TTCTAGTTTT GTCAACTCTG TTGGTATGAG GAATCTCAAG ATTGAAAAT

01T221 120bp  
CCAAAGGAAG TCACATTGTT TTAAGTGTAA AGTACAAGTT CAGAGGTAGA GGTTCCAAAT GC  
C/T  
TAAATTCTTC ATAGATTAGT CTTGCTGAAG TAAAGAATTT GAATAGGGGA CATAGGC

01T222 140bp  
CCTCAGGCCC TCACACACTC ACCTTTCATT ATTCTTGTCT TCTTGACCAT TCTTTATTC  
TCATTAAGGC CACC  
C/T  
CACAAATGAA ACTCACCTT GAGTTAGGTA AAAACGCTCA TAAGCATAAT TTTATCCCT GTGT

01T223 103bp  
TAGGGCATCT TGACATCTGC TTTAGGCACA CTGAAATGTT CAA  
C/T  
GGCAAGAGTA TTTAGGACTG AGAACATCTG ACCACTCAGA GCAAATTATT TGAATTCT

01T224 141bp  
CAAAGCTAAA AGGGGCATCT GAGACAGATT TCCTTTTGTT TTTACTGGCG TGTCAAATGC CAC  
G/A

Table III

GTGACAGCAA AGGAATAATC TTCAGTTTGT GTATAATGAG GTCTGAAATT TCCGTCGCCA  
CATATTGATC ATGAATC

01T228 132bp  
CGCTAAAAAG GGAAAGCCTT CCTTCCTGCC CTAGGACATC CCTGCCAACT T  
C/T  
AGGGAGGTGG GAACCCAGCT GCGCTCTCTA CAGTATGGGT TACTTTTGTG TCTGGAAGGT  
GTCTGACATC CTGAGACCTG

01T230 142bp  
TGAATTGTAC CTTTAAAAAT GGTTAAGATA GTAAATTTTA CCATCTTCAC AGTTTCCCGA  
GATTGCAAGG CCAGCAGTTA AAGACAAAAA CAA  
AACTA  
T/C  
TTCCAACCTGC CCTACAGTGT GCAGACCTTT CCCTTGTCTT GCCCTGAG

01T231 131bp  
TTTTTCAGCAG TGATATTCCT TGCTATGTGT CATTCTATTT GTATGGAACG GCCAAAAGAG G  
T/C  
GAAGCCATAG AGACAGAAAG TAGATTTGTG GTTGCCAGGG GCTGTGGGGA GGGGCCTGGG  
GAGAGATTG

01T232 142bp  
ACCATGAAAA TAGATGACAG AGTAGGCACA GGAAGACCAG TTAGGCCCAT ACAGCAATCA  
AGGTAAGAGA TGATAGTGGC CTGGAACA  
A/G  
CACGTAGCCA TATAGGTGAC TATATTTATA TTTTGAGGGT GATCCAAAAG GAT

01T233 113bp  
GGAGGTTGGA GGGCAGGGGC AGATAGGCCC TACCTTTCCA TAGGGTGAGT GGCAAAGAAT TTG  
T/C  
AGCTATCTTT CACAACAGCT TGGTTAAGCA AAATTTTTTT TTACCATTT  
01T234 130bp  
GGCTATGCTA CAGTCTCTAG CTAAATGGAA GACACATTCA TCCTTCTCC  
C/T  
TCTGACTGCT TTGATCATCA TTTATTGCAT CTCATAACTA ATTTTCTAAA GTTTGGATTG  
GGACTTTTCA GGTCTTTTTT

01T236 128bp  
TTCTCTGGGG GAACCTGTCT CAGTGTTGAC TGCATTGTTG TAGTCTTC  
C/T  
CAAAGTTTGC CCTATTTTTTA AATTCATTAT TTTTGTGACA GTAATTTTGG TACTTGGAAG  
AGTTCAGATG CCCATCTTC

01T237 141bp  
AAAAGGCTAT GGAGGTCCAA CAAAGAACAT CCCAGCTCAG CAAAATGAGT GGCAGCTTCA  
GGTGCGAAGT GGCTCTGATC TAGGCGTTGA GGC  
C/T  
GAGTGGGATT TGGAAGTGTG GAAGTTGTGG GGAGGAGGCA TATTGCA

01T240 121bp  
GGCTGAAAGG ATGAGTGATT TTAAGGGGAA GATTTCCTCA TACTAGCTAG AACCTCTC  
G/A  
TCACGTCTGG CCCCTGTGAG CCTCTGAATG TGTGCTCCCT GGCTGAGCAG CTGATACACC  
CA

01T241 107bp

Table III

TGCTCTTATG TGCCTTTTTTC ACCTCAACAT GCAATGGGAT AATTAAA  
 A/G  
 AGGGTAGATT TTTTTTTATG AAATAGCATT TTAGATGAGG TAATAGAGGA ATACAGATG  
  
 01T242 141bp  
 ATTTGATCCA TTCATTGCTA AAGCAGTAAT TTTGAACCAT ACCATTGCTA AGTACTTAGT  
 CATCAATATA GGGTTGAATA GTTCATCTGA CA  
 T/C  
 TTTTGTTTTA ATTACTAAAA TGTTTTTTTG CCCAGTTCOA TTGGACCA  
  
 01T244 119bp  
 TGGAAGGGAC TGTCTCCCT GCCTGCAGAA TCTGCTGTGG TATCTCTTG  
 A/G  
 ATGAGGCCAT GCAGCCCCCA CCTGGCTCCA CGTTCATTCT TGTCTGATC CTCAAGCACT  
 CAGGGCCTC  
  
 01T246 99bp  
 CTTCCCTTCC CCATTTAGGA CTCTGACGCA GTACAGTTAA TCTGTGCA  
 C/T  
 AGGAAAGAAG AGCTGTTTGA AGAGGTTATT CGGTAAATGC AGAGAATGTC  
  
 01T247 143bp  
 AAAGAAATGA AAATGAAAA ACAGTAAATG AGGGAAAGGG AAAATAATGA TGGCAAGGTA  
 AGGAGGAG  
 C/T  
 TAGAAGGTTA TGCAAACTA GAGTTATGCA AAAGTAGGAG CTAGAAGGTT ATGCTAGAGG  
 TTATGCAAAA CTCA  
  
 01T248 120bp  
 GTTCGTGGAA GCTCACTGGT AGGTGAAGAT GCTTTCTGAG TGATAACATA TGAGCTATTG  
 CAAACATGGT  
 C/T  
 GGGGATTCCA CATGCCATTT AGCAATAACT TGGGGATAAT GTGGTACGT  
  
 01T249 149bp  
 TGGCTCTACT TTCAAAAGTT CTTAATTTTA ATATAGTCAA AACTATTTTT TCTTTGGTGG TAAAT  
 A/G  
 CTTTTCATGT CTTTAAAAAA ATCTTCCCTT TCTCTAAGGT TTGAAGGATA CTAGCTTAAC  
 TTCTTCCACA GGTTTCAGAA TTT  
  
 01T250 136bp  
 ATACCATTCT ATCAAAGAAC GGCATTTGCT TTTTGTTACA CAAATTATTT CA  
 A/G  
 TGTTTAAGGA CAAAATGAAA CAAAACAGGA AAACCAAATT AACAAGAAAA AATTCCCTCT  
 ACAACCTTAC CCCTGCCCCG CCC  
  
 01T251 109bp  
 AAAGTGATTG TCAATATGGC AAAAAAGTTG GAGAGTGAAG TGTTTCAGTA TATGGATCTT G  
 G/A  
 AGAAATTCAA GAGCTAATAG AACTACGCA GGAGACAACT TGCTGGA  
  
 01T253 141bp  
 TCTCCAGAA TTCCCAACAA CCAAGGTTG CATTAAATTAC TTTAATGGC AAAACCACTG  
 TTAATTTTGC ACCAA  
 C/T  
 CTAATATTAA CCTATTGTGG GAGGGACCCA TGGGGAGGTA ATTGAATCAT GGGGCCAGTC  
 TTTC



01T255 139bp  
 TCCTAAACTG AGTGTATGCA GTAGGTGGTC AACAAATATTC ATTAGTA  
 A/G  
 ATTCTTTGTA TTCTTCCTGA GGGCAAACT GCTAAACTC CCTGGAGAAA AAGGCAATAC  
 CTGGCAAACA TAAGGCATCT CTCCAGGCTT A

01T256 139bp  
 CTTTGTGTTA ATGGCTGAAC AACTGTACAT ATCTGTAAAA CTCATTAAAG TATATATTTA  
 AAATGGGTGA ATTTTAATGT AGGTAAATTG TACCTCA  
 A/G  
 TAAAGATGAA TTTTTTTTTT AGCTGAGCGG GTGCAGAAAC AGTAAGGAAT T

01T257 114bp  
 CTACTGTAGC AGAAAGCCAA TAGAAAATGT CTAAATTTTA TCACTAGGAA GCAGCAATAT  
 A/G  
 AGCATATTAT TTAGGAATAT AATAAGACAT CTCGAAGAGT TGACAGTGGT TGT

01T258 115bp  
 CACTAAGAGG TAAGGCAGCT CAAAGGGCGT TGGCTAATGA AGTGGATTAT TGGGAGGG  
 A/G  
 TTTACTCTTA CGGGTTTTAG TGGGGGAATA CATTAGGTAA GATGTCTGCT GGGAAAT

01T259 137bp  
 TCAACTTGGT GACTTATATA TGGAGAATTT CAAATATGTT CTAAGTGTTT GCCTATATAT  
 TTTTGGTCTG ACATGGGGA  
 A/G  
 AGAAGGTTTC TAGGGGAGAC TAATCTCTGA GCACTTACCA GGAGAGGACA CCTAAGG

01T262 139bp  
 AGAGGCACTT TCCACCTGGT TACCAACCAG AGTGGTAAGT GGCCATTGAA C  
 A/G  
 CTTTGGATAA CTTATTAATG GATGTATATG TGTTATTCTG CCTCTTCAAA ACCAGAGGAG  
 GGCTATGCTG TAATGGGCTT AGATCTA

01T266 149bp  
 GCCCTGAGAC TGTCTGCTAA TTTGGATTCT AGAACACAC AATCCACCTT ACAAGTA  
 C/T  
 GTAAGGAGGA AAGTAAATAA CAAACGGGTA AAGTGCTTTG TAAACTGTCT ATACAAATAT  
 AAGAGACCGT TATTACAACA CAGCGGAAGA A

01T267 97bp  
 TAGAACACAC TGCCCGCAAT ACCCCCCCTT TCTTGCTGCG CCCTGC  
 A/G  
 GCTCCCGCGT GGAACCTCAT TCTTCCATTT GCCCCCGCC CCCAGTTGCT

01T268 108bp  
 CTTGTGGTGA TGGATATCCT AAATACCCTG ACTTGATCAC TGCACATTCT ATGCATGTAA CAAA  
 T/C  
 ACTCACAGGT ATCCCATAAA TATGTACAAA CTTTATCAAT AAAACATTTT TTAAAAAGAT  
 GTGCTTCTGA TCA

01T270 132bp  
 GGGGACTGTG CCTTGACACAC CGGCCGCGAC CTAGCCCTCT GCCCCCACT CAGTACTTCC  
 ATTAGTCCC GTGGAA  
 C/T  
 AGGAGAGACC TGTTCCCAAT CTGGCCGAGA AACTAGGGAT GGGGGGACTG TATTG

01T271 149bp  
ATTGAAGAAG AAAAAAGAAC AAAGTATTTT TTCCCCATGT TTTCCTGGTG TCTTTTTTCAA  
AGGTTTGTGT CTTAACAGGT GCCAAGAGCC TGCAATC  
C/T  
TTCCCAAACA GCCCTTTGTT CTGTGCTCAA GTCAACCCAC TGGGACTTTA C  
01T272 124bp  
CTGACTCCTT TCCCTCAACA TGCAAGCATG ATCAAGCCTT TCCCATTTTA AAGTAAT  
C/T  
TTCCAACCTTA CCTCTCCTTT CATCATCCTC TCTCTTTGGC CTTACCATCT TAGCGAAATT  
TATTGA

01T273 149bp  
CCCAGAAACC TTAAATATAG ACAGACTTTA TTAATTTATG TAGGAAGCCA AAAATAGGAA  
ATAAAAAGAT C  
C/T  
GGAGTTCAGA TATACTGATA TATTCAGCAA CTGAAACTTA CAATTCCTTC AATTCAGTCA  
GAGCAGAGAC ATTTAAA

01T274 145bp  
CAAACCTTGAA GGACTCATTC TGAGGCAGAG AATGAATAAA TC  
A/G  
TTACCTTTGT GAAGCATCAG AATCAGCAGC ACTTTCCTGT CCCAGGAGAA GAGGGAAGGG  
GAGGATGGCA CGTTTCAGGG CTTAGGGGAG GATAGGGGAG AA

01T277 105bp  
CGCAAGCCCA GAAAGACGGC TGGGGGCAGG GGTGCTGCGT ACTGTTCAAT GAGAGCCATA A  
T/C  
GTGGCTGTAA CTGTCTTCCT CATATTGCAA GAACACTGCT GGC

01T278 124bp  
GGTGAATCAG GAAGATTTCT AAAGTCCTAG TTCTACAACT AAAGCATTAG ACGATTAAGG AAG  
C/T  
CCTTGATATT CTCTCAGAAC TTTCAGTGAC CTTCTGCCCTC CTACAGACTT CGAGGAAGAG

01t279 142bp  
GCTTGCCTGT GCTGCTCCCT CTGCCCACTA GAGGGAAGCC CAACCTCAGG CTGAGGCCTA  
GAAGGGGA  
C/T  
GGCTGCGCCA TGTGGGGCAG GGACAAGGAG GGGAGGAGAT GGCCTGCCAC TTCCAGACCC  
CAGTGCGAAA ACC

01T281 149bp  
ACCATCAGAT CTCATGAGAC TCATTACTAT TACAAGAAAA ACATGGAGGA AACTGCCTCT  
ATGATTCAAT TACCTCCACC TGGTCC  
C/T  
ACCCTTGACA CACAGGGATT ACGGGGATTA CAATTCAAGA TAGATTTTGA GTAGGGACAC  
AG

01T282 145bp  
AGGACTGCCA TTTTCTAATT CAGCAAGAAG TCAAGAAGTA TAGGATAGGT GTGAAGGATG G  
C/T  
GAGATCTGTA AATGTGTAAG CTTCATAACT TCTCTGTGAC TTGCTTAGCT TTATTCTGTT  
TTTTTTTTTG TTGGCAAAC GTA

01T283 137bp

Table III

AGCCGGTTGG TCTGGGCAGG AACGAAGTCT GTGTGGTCAA AGGGGACCCG CGCCGGCGAG  
 ACTGGGATGC TG  
 C/T  
 TTGGGCTGGG CGGTCAGAGT ATGGAGTGGG GCTGGGGTGA GGTGGCAAGC ACCCCAGGGT  
 GGGA

01T285 149bp  
 GTAGAACCAT GAACCAATTA AACCTTTTTT AAAATAAATT ACCCAGGTAT TTCTTTATAG  
 CAGTGCAAGA ACAGACTACT AATACACCTA GAGACCCA  
 C/T  
 GGGACACCAT CAAGCAGACC AATAGATACA TAATGACGTT CTAGAAGGAG

01T286 110bp  
 GGTTTTATGC ATTTCTCTCA AACACCGACT GCTCTTCACG CACTTTCAAA CCATATT  
 T/C  
 CCTGTTCTCG CAATCCACTA TAGTGATCTG ATACATTAGA AAGCTGCCCT AG

01T287 122bp  
 GGTTACCAGA GTTCCAATTC AATTAACACA ACTAACTGAC TATTGTAACT TGTAGACATT  
 ACCAATGGGA ATTAAC  
 A/G  
 CTTCTGAAAA AGGTTTATTT CTTCTCTTGA AGAAGAGATT GGGAGGAAAG GTATA

01T288 121bp  
 GTTGAGCATT TCAAGATCTT TCTCAGTAAT AAAATAAGTA AAGTATTTTA AAAATAGAAG TT  
 C/T  
 TCAATAATCA ACAATTGAT CTCTGTTGATA TCTATAGAAT GCTCTAATTA ACGGAGAA

01T290 125bp  
 GTATGCTCAT TAAACATTA TTCGTTATAG AAAAAAGTC TCATAAAATC TGGAAGCAAA  
 TGAATGTCA  
 A/G  
 TTAAGAGATT ATTTTTATCG AATGGAAATA TGAATCAGCT TAAATTGTGC ATTTC

01T291 146bp  
 CCCAATCTAA ATGTACATCA ACTGGTAAAT GAATAAAAAC ATGTAGTACA TCTATACAAT  
 GGAATATTAT TCAGCAATA  
 A/G  
 TAAGGAATGA AACACAGATA CAAGCTTGCA CTTTTATAAA CCTCGAACAT TATGTTGCAT  
 GAAGAA

01T292 121bp  
 ACTATTCTGT TCTAAGGTTG CACTCCAGGT TGAAATTGGC TGACAAGGT  
 T/C  
 TTAGCTTGGG TAGGATTTAT TCCCATATA TTAAATTATT TTTTAAATTA GTTCAATGCC  
 CAGGTCATTT-C

01T295 116bp  
 CTATGTCTGT CCCTTGCCCA TTTACCCGCT ATATTCTGTC TATATTTTC  
 A/G  
 CTGAATTTGG GTCCTGCTTC TTATGCTTTA TGACAATGTG TGGTACAGCC CTTTGAATCA  
 CTGTTT

01T296 143bp  
 ACCTGAAAGA AAGGAAATCA GTATATGGAA GGAATACCTG CACTCCCATG TTCATTGCAG  
 CACTATTAC AATAGTCAAG ATACAGAATC A  
 A/G

Table III

CCGAAGTGCC CATCAGTGGG TGAATGCATA AAGAAATATG GTACATGTGC A

01T298 117bp  
 TTTCTGGTTG CAGCACTAAA AGTCAACTTG CCTTTTGTG GCCTGC  
 A/G  
 TTGACCATT TCTTCACCAA CTAAACACTT TCAACAGAAT AGATAAACTT GAATCCTAGA  
 TGAGATAGCA

01T299 142bp  
 ACATAATACA GCTGCCACAG CCCTATGTCA TTAAGCAGTT GAATTAATCA ACCACTTTGC  
 TACCCACCTC TGAACCTTTT GCTTTTGGAG ATAA  
 C/T  
 CCCCTTTTTG TTTAACCTAT TTTGTGTTGA ATCCTTACTT ACTCAAA

01T300 124bp  
 TCAGTGACCC ACAATCCATT CCTAAAAGGG AGAGCCTCCT GTCTTTCTCT CAGTTCCTC A  
 A/G  
 GCTCTTAGCA GGACTCAATA AGAGCCCCAG AAATTTCCCA GAAGTAGGTG ATTTAAAAAC  
 AC

01T301 124bp  
 TAGAGTAAAT GTGGTCTGCA CAGGTGTAGG AAAGAGTGTG GGAGAGGAGG AGGGGACAA  
 C/T  
 CTCATGCCTT TCTTTATTAA AAACACATAA AATAAACCTT ATAAAATGAA AAAGTTCCAT  
 GGAT

01T302 103bp  
 GGAGCATTTT TTGGTATCTT TATTTTTTAG ACCACATCCT TCATGGTTGC AT  
 G/A  
 TTGTTCTATT TTCTTAGGAA TGCCTGAAG CTTGGCTTTG CTTTATGTT

01T303 90bp  
 AGGATGCAAC AGGAGCGGGG TTGCCTGATA AGACAGCGAT AGAAAACC  
 A/G  
 AGAGATAAAG GAAGTCTGGC CAGCAGCAGC TAGTCTAGAG G

01T305 106bp  
 GAAGGGTGTG TGCAAGTGTA GAACAAATTC CTTCCGTGAT TAGTCAAGCT ACCTGACTT  
 T/C  
 AAACAAGTTT TATTTTTGTC TCTATTACTG TTAAACTGCA TGGCCT

01T306 115bp  
 AGGCTGAAAT GGTGTATGT GATTCCAGAG GCCAAAAGGC TGGTGTGGAG TCA  
 C/T  
 GGCAACTTTC CTACCACTAC ATTCCCCCTT CCTATGAGTT TCATCGTACC AATGATGGCT  
 G

01T307 115bp  
 ACAACTGTGA ATTGTGGCCA AGTCTCCCAA ACTGGTTTTG TTCAGTTCTG AACTTGCAA  
 C/T  
 ACACCAGAAA TTTTAGGGTT TGGAAATTAG GAGATCAAGA GTTTGAATGA AGAA

01T308 115bp  
 CAGACCAAAA TACATTTATG ACACCTGTGA AAGTAGAGGA AGAAGAAAGG TTTGTGTAGG  
 AAGAGTCTCA GA  
 C/T  
 CAAAAATCAC TTCTATGAAA GTTTCAGCCA GGGCCAATGG TG

Table III

01T309 131bp  
 AAGAAGCCTC CAGGAAAACA CATCGCTTGC TCCAGGAGTG TGTTCACAGA GTGTCGACAC  
 AGCTCCAGC  
 A/G  
 TTTCTCACAG CCTCTGCTGC CAGGAAAGGA TAAACACCA CCCATATTCA GGAACAAAGA  
 C

01T310 135bp  
 GCCCACCTTA ATGACCTCAT CTTAACTTGA TAATCTGAAA GCACCCTATT TCCAAATAAG  
 GTGACATTCA  
 G/A  
 AGGGTGTAG GACTTCAATA TCTTTTGAGG GGACACAGTT CAACCCATAA CACCTACCAA  
 CGGT

01T312 145bp  
 GACACTCTGT TGAGATGGGG GTTAGACATC TAGGTACTGT TCCTGTTTAT CTACT  
 A/G  
 ACTAGCTACA CAATTGTGAG CACATTGCTT CTTTATCTGT TTCTCTAAGT CCTTCTTCAT  
 CAAAATAAT TGAATTTCCA TTTTGCTGG

01T313 134bp  
 CAAAAGAAGG AACAGGGAAT ATACCTAGAC TTTAACCTTG TT  
 A/G  
 ATACTATAGT ACCTGTCCTG AGTAGTACAT TGTAGAGGCC AGCCTGACTA ACTGGAAGTC  
 AAAGGAGAAA TACCAAGAAG AGGAATGGCC T

01T314 110bp  
 AGGGGAGAGT TTCTTTTTTAA GTTATTATTT CATATTTTAT GGATTTTATG TCTTCCTCTG  
 TCATTT  
 C/T  
 CTCCAAGCTC AGTTTGGGGA ACCAGCAGTC TGTGTTAGTT CAC

01T316 143bp  
 ATCAGGCTCT ATTAAATGGT GGTAGGATAT GAGGCTACAG ATAACAGCAA AAAAATTAAT  
 CAAAGTTTCA ATTA  
 A/G  
 CACAGTACAC ACAGATCAAC CCACCAGCTA TTATGTATTA GTTTTAAGCA CTTGTCATTA  
 TGCCTCAT

01T317 146bp  
 TGGAATACAC AAATTTTGGG AATAAAAGGT TCAAGTTCCA ACATGCCAAA ATT  
 C/T  
 TACTGAAAGT AACAACTATA TTAAAGCTTG TAGTGACCAG GTACAGTAGC TCATGCCTGT  
 AATCCCAGCA CTTTGGGAGG CTGAGGCGGA TA

01T319 136bp  
 GTTTACAAAT GAACTCCTTT TCTGTCTTTG CATTTTAGAG AAATAAGTG ACTAAGGAGG  
 AATGTCAAGG ATCATAGTGA CAA  
 C/T  
 ATGTTCTTCA AACGAAGCTA GGAGACTGAG AGGGAAGTGA TGGAGGGCTG AC

01T320 145bp  
 TTTGGCTCCT CTATGGGCAC AGCTGGCTCA GAGGGCTCTG AGCAGCATCT TTCTATTCTG  
 GGAAACTACA GCCAC  
 G/A  
 CGCCCGTGTG AGCAAGTTTG CACCATCACG CTCTGAGACC AGAGTCCTGC CCTTTCTCCT  
 CCTCTGTGC

Table III

01T321 133bp  
GCACTTGTTA GAAACACGAA ACTCGTGGGC CTGACTTCAG ACCTACTGAA TCAGAAATAC  
TGGATGGGGC TCAGCAATTT G  
T/C  
TTTTAACAAG CTCTTAGCTG ATTCAGATGA ATGCAAATGA CTCTTAACCA C

01T322 141bp  
TCTTTTGATC AAAGCAATTT TTACTTAGAA GGAAACAGCT GACTTACAAA GAAATTGCAC TGAG  
A/G  
CTATTTCTAA ATAAAAGTGT TTTTGCTGTG GCATTGCAGG GAATTGAGGC ACCTTCCATA  
CTGGTGGTTA CTTACA

01T323 118bp  
AGTTTTCTAC AGAAATCACT CAATGAGCAT TGATGGCCTG AAATGAATTT  
C/T  
GGCTTAAATG GTACAAATGT TCAGAAGCAG GAAAGCTCAG GGCAGGTTTG AGGAAATTAA  
GCAGTCC

01T324 129bp  
CAGTTGAAGC CACTACAACA TCTAATACAT CAGCCTTGGA AGCCATCTTG CAGATCATCT CATC  
A/G  
TGGGAAAACA CACAATATCG ATGAAGCAAG CGATAATGCT CCACACACTG TCGGCCTAAT  
GGCA

01T326 133bp  
GCATAACCCC AAAGGGTATT CTTAGGATTT GTAGGTAAGG GTTTGAGAAG  
A/G  
AATATGTCGG CTTAAATATG GAGAGAACT TTTAAATGCA GTCAATAGAT ATGATGGACT  
GCATTAAAAAT ATGTTGAATT CC

01T327 132bp  
TGTGCTTTGG TTTCTTCTCA GACTGAAAGC TGGACTAGGG AGACAAGTGC TAGAAAATGA A  
A/G  
CATAAAGCAT GAAGGGTATT TTTTTTCTCC GTTAAAAGAA CATTACACG GTCCCTAGTG  
TCTACAAAAG

01T328 146bp  
GTGTGTCTCT GACCTGGGCT CTGATAATAG GACCCAAAAT CCCATCTTCT TTC  
A/G  
TATTGGGATT CACTGTATGT TTGGTGAAGG ACTCATCTTC GTACTGTGTG TACATAACTT  
TCTTATAATG TTTTCCAATT TGGTTTGAGA AA

01T330 111bp  
AGTGACAACT TAGACATTTG GTGAAAACCT ATTTTCATTT TATATG  
A/G  
TAGCAGCAGG TTGTGCAGGA CATGAAGGCT ATACAGTTTT GTGAGGCCTC CTTAAGTAAA  
AAGT

01T331 136bp  
ACCACTCACT CTTTGGGTCC GTGCCATCTT TAAGAGCTGT AACACTCACC GC  
A/G  
AAGGTCCATG GTTCATTCT TAAAGTCAGT GAGACCACTA ACCCACTGGC AGGAACGAAC  
TCCAGACACA AGATGATGGA AGC

01T335 139bp

Table III

CAGCTTCCAG AGACAGGCTT TTGATCACCA CAGGGTCCTT CCCTTTGTCC CAGTTATCCC  
AGGGAAAGCT ACTAATCTGG TTCAGGTGG

A/G

CGTGGGCAGG GGCTGCTAGG CCTGCAAGAA GCAAGCCCAG GACAATCAG

01T336 134bp

AAGTTGAATT TAACAAGCCT TCTATTAGAC TTGAATGCCT GCATTATGAT AATTATAAGC  
ACACCTTTCA CCAGT

G/A

TAATATTTTT CCTCTTAGGA GCTGTATGGC AAAAAGAAGT TTTGTGAAAT TTTATTGC

01T340 127bp

CCATTCTAAC TGGTGTGAGG TGGTATCTCA TTGTGGTTTT GATTTCATT TCTCTGATGG  
CCAGTGATGA TGAGCATTT

T/C

TTCATGTGTT TTTTGGCTGC ATAAATGTCT TCTTTTGAGA AGTGTCT

01T341 108bp

GAAGCTGAGG GAGCCCTGGG GCGTGGGAA ACAGCGCTGA CAGTTAGAC

C/T

GTAAGAGCCC AGGGTAGGAA CTGGGCCTTT CGCTCAGTAC CTTGGGCCAG GTCTGGCA

01T342 149bp

TTGGAGGTAT CATCTTGACT TCTCTTCTGG TCATGGCTTG TTACAGATTT GGCACTTTTTC  
ACTTGAC

C/T

TGAAAGGAAA CAGATTTTAA AATTACATTT AATTAGTTG CAATATGAAA CAAAATGAAG  
CCAGTTTTTA AGACAATAAG A

01T343 109bp

AGTTTCAGAG TTCAGCTTCA AAGCTAAATG TAATCCCCCG TCTC

C/T

CCTTCCCCTA CAATAGTAAA ATGAAGAAAG CTATTTATTT CCAA

01T344 113bp

TTTTGAAACA TGCAGCGCAA AACTCAAAT TTCATAGATT GACTTTGTTC TTAACAGAAA  
ATCTCT

A/G

TGAAAGGAAA TTTGTGAAGT AGCAAGAGAA AAAGAAAAGC ATGGTG

01T346 132bp

ATTAACATGG AAGGGGAAAT ATGATAGATA TATAAGGACC CTCCTCCCTC A

T/C

TTATATTCTA TTAAATCCTA TCCTCAACTC TTGCCCTGCT CTCCGCTCCA CCCCCTGCCA  
ACTACTCAGT CCCACCCAAC

01T349 126bp

GTGATCCTTT CAAAATGGA TTCAGAAATC ATGTCCTGCT TCTGCCCAA GTTCCC

A/G

AATGACTTCC CAGTCACTCA GAGCACAAAGC TGACGCTCGA CACATCTGGG CCCCCTAAGA  
TTTTCATTT

01T351

ATTCCAAAGTTTTAAATTTTCCCATTCGTGTCATAGTTTGGGTACCCTACTCCTCAGACC  
CGGGGCGAGCCTTCGGCTGTGACTCAGCACATAAAAAACCAGAACGCCGGAAGTATTTTC  
CTACACCCGCCGGATG

A/G

ACGCTGCTCCCGAGCGCCGCAAATACTAATTGGCTCTTCTCTACCCTACAGTCGGCCCCGA  
CAGTGGTGGGGTTTCATCCTCAAGCCCTAAGAAAGTGCTAAAAAGACCAGTCTGGATGTG

01T353 110bp  
AAATTGTCTT GGAGAAGCCC TCAGAAGAAT AGGGATAGTC TGTTTGAGCG TGTTGTCAAC C  
C/T  
TCAGTCCTCT CTTGTGATCC TAGTTAACCT TCCCTGGTTG ATAAGATTC

01T354 102bp  
CTCTCCTCAG GCCTGACTGG CTATGTATTT TCATAAGTGA AGAATTT  
C/T  
CTGGTGAATT CATGCGATGC GTTCATCAGA GAATAAGAAA CGCAAACCAT ACTG

01T355 142bp  
AGGTCTCATC TTCTTCATGG ATACAGTAAT GCTAATAGAA CCCTCCTATT CCATAGTGT  
C/T  
GGCTGCTGTG AAGGAGAAAAG GCAATACATG GGCTACATAT TACATAATAC TATGTAAGTA  
TTAGCCTTAT CATTATGGGG GC

01T359 113bp  
TGTAGGTCAC TCTATCTCTT CAAATACCCT TTAGTGGTAT TTAAGGTTTT TGCAG  
A/G  
GTCTGGGGAC TTAGGTGTTT CAACTATCAC CATGGATTTC CAGATTTTGT AAAAGGT

01T361 123bp  
GAACAGATGG TAGCCTGTGG TGAAGGTTCT CTTTCAGATC TTTAGTCTCT TTCC  
C/T  
GTGAATTAAT CTTACCTAGA TCTGGCCAAG AGGAGCCTCA GAGTAAGCCT ATTTGCATCT  
GTTATTT

01T362 117bp  
TTTCATTAC TTTCTCTGTG CTTAACAAGG CAAAGGGATT ACTGTGCT  
G/A  
GGGTTACTGC TATACCAAAC TGTCATCTCA GTTCTTCTTG GATACAGTCA GTTTAATTAT  
GCCTGGTT

01T363 141bp  
AAAACATTCT GCCAGTTATG GTCAGGGAAC TGCATATTTT TAGCTTATCT TCTTCATTGT AAA  
C/T  
TCTCTAACAC CTAGAACTCT ACCTACCCAT AGTGGACACT CAAAAATAAT TTGCTGAATG  
AATAGTAAAT GTGGACA

01T364 135bp  
GCGCAGGGAA TACACAAGGC TTAATCCACT AACAGAATAG GTTGAAAATA C  
T/C  
GAGATTCACC CTCCACCCCA ACAATGCAAG GAGACTCAAA GAAATTAATG ATCACAGGCT  
GGGTTTGTGA TGAAAGGAAA ACAA

01T366 129bp  
GCTGCAGGGC TCTGCTGCTG GTCACCCACG CTGCAAAACC CAAACCT  
C/T  
CCTCTACTGG GCCCTCAGTT TGCGCACATA AGGAAACCCA TTGCCTTCCT TTAATCAGAC  
TAGGGCTCTA ACCTAGTGAA C

01T367 147bp  
GAAC TTGGAA ATTGATTTGC ATCTAGTAGC AGACAGGGGC TCCCAACCTG AGCACAAC  
A/G

Table III



TACCAGGGGA ACTGTGGCAA GAGGCTGTTC TCACAGTCTC TTCCTTGGC TGAGGGATAG  
GCCTAAAAAG ATGGAGTAA CGACTCCA

01T371 122bp  
TCATATATGC ACATTGCATC CTAACCACAC CAGACTTTCA AGAGCCTTTG CCTTTGTTTT  
TCAGAT  
C/T  
TTAAACTAAA TCTTATCTAA CACCACCCCA TCCAGGACCA TTTTGTTTTG TTTTT

01T372 114bp  
AAAATGTCTG TAAATTACAG CATCTATAGA CAGCTATGTT TGCAACATCC CTTTAACCAC  
G/A  
CTATGATATT TGCTAACCAT GCTAGTGCTA TTTGTTCTTA TTACAGACCC AGA

01T373 125bp  
TGTAACATCT AATTTGTGGC ATTGAGTAA GTTTAAGACT TGTCAGACCT GCCTTGG  
A/G  
AGGGATAGCT TCCCCACCCC TTCCCCAGCC ACAAATGGAA TACTGCATTC CACAGTGAGA  
ATGTGGC

01T375 104bp  
CTCCTCCATC CACTTAAGGT AATCACAGCA CTGTAAGGGG CTATATCAAA ATTC  
G/A  
GCATCAGCAA CATAAATTTG GTTGACAACT GAGCTGAATA GAGGACCTA

01T376 128bp  
GCCATAGACC TCTGCAAGCA AAGCGACCCC AAGCATTTCT TTCTGCCTGA ATAATTA  
C/T  
GGTTCAGTTC ATCTGTGATG AGAGATATCA GCCCTGCCAC AGCTAATTAC TATAGGAATT  
GGCCTTCAGT

01T377 131bp  
CTGAAAAAGG TCTCTCTGGC AACAAAGGCAA CAAGGTGGAC ACTGGAATGT GAAGGTGCTA  
GAAGAC  
C/T  
ACAGAAAGTG TATTTAGAAG AATGGCAGCA GCCTGGAAAA GCAAGGATGG GGAATGAACC CAAG

01T380 127bp  
CCATGAGGCA GATAAGGGAG TATTTACAGA GGTAGGTAC ACTGGACCTA CCT  
C/T  
ACGGGCTTGT TATAAGGTTT GGTAACATTG AGAAGCTACT AGGCATCACT GCACTATATG  
CATTCCATAT GCC

01T381 126bp  
TGAGAATTCT GGCAAGATTT TATTTGATGA AAGTATTCCA TGGTAGTAGA ATACTATG  
C/T  
GGCCATAAAA AAGAATGAGA TCGTGTCTTT TGCAGGGGCA CAGATGAAGC TGGAAGCCAT  
CATCCTC

01T382 135bp  
ATCATCATTC AGCATGGATA TTATCATCGA AATTTAAGAA AAGGTATG  
C/T  
TATGTATTTT AATGGCCTCT AGTGATTCTC CCAGTCCTAA GATTCTATCA TAATTTTAAG  
TAAAGAATAT GCCGCATGCA TAATTT

01T383 113bp  
CTAACACTTT CCTCTTCATG GGGATAACCA TATCTGAAGA ATGTTAC

Table III

A/G

TAAGTGCATA ATCGATGCTT CCTGGACCCT CAGCCCAACT TTAGATCTCT GGGGGATGGC  
TTTA

01T387 149bp

TGTTGAGGAG ATGGGCACCT AATTGAATGC TTAAAAGGAT ATTTTTCCTA AGCTTTTCTT  
GAAGCTTAGT AT

C/T

ACTTCTTAAT CACTGTACTT GACAAGTCAA CCTTTTAATC GGAGCCTGAT AAATCCATAA  
CATAAAAAAT TGCATT

01T388 140bp

CTCCCAGTAG GACAAGGGAA AGAATAAAAT ATCTTATCTC CCTGTAGTGA GAC

A/G

GCTTTATTAA GATTTGACAG TAGTTATTTA ACAGCAATAA TTGAGTTTAA TGCAAGATTA  
TACACGTTCT CCTAATCTGG CATCAA

01T389 149bp

CCAAACCTGC AGAGAACCTA TTGGTCATTA GCGATGAGAA TGAAGTCAAG TGTTTATTAC  
TGATTCACAT ATAATAAAGG TGAATAACAG GGTG

G/A

CTCATAACCC AACAACTCTG TCTCCTCAAC CTGGAAGTCT ACGCCTTATC AGAG

01T390 124bp

CCAAGGGTAT TAGTCAGCTC AGGCTGCCAT AGAAAGATAC CATAGGTTGG GTGG

C/T

TTAACAACAG ACTTTTATTT TCTCAATATT CTGGAGGCCA AAAGTCAAAG ATCGATGTGC  
TCACAGAGT

01T391 148bp

ACAATCACAA GGTCACCAA TAAGCTGTCT GCAAGCTGAG GAGCAAGGAG AACCAGTCTG  
AGGAGCAAGG AGAACTCAGG AA

T/C

TTGGAGTCTG TTGTTTGAGG GCAGGAAGTA CCCGGCATGG GAGAAAGATG TACACCAAGA  
GGCTA

01T393 141bp

CCCTATGATG TTCCCTCTCT CCCCTCAATG ACTGTAGCTC TCTAGTTCTC TTTCTACTAC  
ACATTCA

C/T

CACTTAATAT TTTGTACTGC TTTCTTAACT GACAATAAAT GCTGGCCAAT GCTTTCCCTG  
TTTGTGCACA ATA

01T394 137bp

TTCTTTAAAT CAAGCACAGG GCAACATTGA ATACATTTTC CTACTTTATA TAGCATTTCT  
GCAAGTGCTG GGGTTACATT TTAGTCTTCA

C/T

AGAATGCGTG ATTCAAAAGT TTATTTTTTT GATTAAAGA CACGAA

01T395 117bp

GATTTTTGGA TATGGTGAAA CATAGAGGTC TAGTTTCATT CTTCTGCATA TGAAAATCCA  
GTTTTCTAG AAC

T/C

GTTAATTGAA GAGACTGTCT TTTCCACAAC ATCCCTTTGT CAA

01T396 133bp

GGCTGAAATT TCACTTCCTC AAAAGAACAT TTTCTTGACC TCTAACA

Table III

C/T  
TCTAAATCCC ACCCACTCCC TGCTTCATGT ATCTCTTTTC TGTAGCACTT GCCATAGTGT  
AGGTTTACCA TGAATTAGTG TGATT

01T397 145bp  
CCCTGATATC AGCTAGGGGT CATATGGATA CTGGCTTGCC C  
A/G  
TGTGCTAGAA CTGGGCACTG GGATGAAGGA ATTACTTCAA CATGTGTTTG GATAGTTCTA  
CCCACCTTTT GCAAGGAGGT TGGTTTGTGC GTCTGCAACG ACC

01T398 149bp  
GTCCCCACAC TGGGCTTCTG GACAGGTGGC TGCCAAGATG GGGGGACCCT GCCCC  
C/T  
GAGGCCTCAC CTTGACGTTG TGCATGCTCA TGAGGTTCCC ACAGTGGTCC AGATACTGCT  
TCAGGTCAC TGCCTGGAAC ACAGAGCGTG GCT

01T399 144bp  
AAGGCTGGGA GGTGCCCCCA TTCTCTGGGT TGGAGCGTGA TGGC  
A/G  
TCATCTATGG TCGGGGCACA CTGGACGACA AGAACTCTGT GATGGTCTGA GATGCAATGT  
TCCCTCTGCC TTGGGGCCCT AAAGATCAAT CAGGATGGG

01T400 147bp  
AAGCTCTGAC TTGTCTTGG CTGCAAAGAC CTGAGGTCTT CTCTTTCTAA GGCTCCTA  
A/G  
AAAGTGTCTT CTTGCAGCAT CTTGGCCAAT TCTCACTGGA GTTCTATTTG GAACAAGTAC  
TAAAATGCAA GCCAGAGTCA ACAGAAGA

01T403 131bp  
TAAATAATCC TGCAATAATT CCTGAAAAGT TGTAATCAC TGACA  
G/A  
TGAGCTTGGG GTGTTATCTC TCTCAGGGAC ATTTGTATTT TAATAGGAGT CTCATAATGC  
TACAAAACT TTAATCAAAG CAATT

01T404 137bp  
CAGCCACAAA TCTGGTCAAT GAAACACACC CAAGAACCTG TAAGATTATA  
T/C  
GCCAGGTTCC ATGGGAAGTG CACTTGAC T TCTCTCCCAA GCAGTGAGTA GACTGAAAGT  
TTCCAAAGGT GGGGTTTGT GTTACC

01T406 125bp  
AACCACCTGA TGACGTGTGT ATTAAACAAA CAAACATTTT GAAGTGCATT CTTTATAAGG  
TAAGGCTTGG GAGGAAAGC  
C/T  
GCCCACAATT AACCTAGGAA TTAAAAAGGT AAGCAGAAAC AACTT

01T408 124bp  
GCCTCAGTTT TCCCCACTGT ACCATGAGAA TAGTAGCTGT ACCTTTCTCC TAGGGTTGTT  
GTGAAAGTTA AAT  
A/G  
AATTAAGGTG TACATGCTGG TGCCTGACGC ATAAGTGTGC TACATGTGTG

01T410 109bp  
CTGGGCACTC CCAATTTCTA GTCATTCAAT ATCTATTTTT CTCCTTCTTT TCTTCA  
A/G  
ACCTTGTGTC TTTCATTTAG TTTCTCAATT CATACAAAAC CGCATCCAGG AC

Table III

01T411 148bp  
 CAAACCTGC AGGGCCAAAA CAAATACAAC GCATCAGAGG CCCACCTCC TAACCAAGGA  
 AAGGGTAAAG GCAAGAATAA CACCAAGAGG CCACCAGCC  
 T/C  
 CCCATCAGAC GGGCAGGACC ATGGCGGCTC CTAGCACATA AGCCTCGG

01T412 104bp  
 TAAAGCATT CCAAACAAAC ACAATTTAGG ACAATTTGTG ACA  
 C/T  
 ACATTTGCTT TAGCTAAGAG ATGAGGATGA TTCAAATTG AACCATAACA CGAACATATC

01T414 121bp  
 GGGAGATGAA GATGACCCTA TGTACATCTT CCAGTCCAAT TATAAGGCA  
 C/T  
 ATATGGCCAG CCATGTGACC CACATGCCCA TAATCAACCC CAAGGAGAAG TACAAGCACC  
 TAGCCATAAA G

01T415 133bp  
 TCTGGGGATC TCTTAGGTGG CTGGTGATTC CTCAGAGCAT TTTCCAC  
 A/G  
 CTTACCAGCT TTTCTATTAA AGAGGTTTCTG ACTGTGCTTT TCTGTGCAGA AATGTTTATG  
 TCTTTTTTTT TTGAGACAGG GTCT

01t417 134bp  
 GCACACATTT AATTTGTTTG CACCAAAAAA GAACAGTAGA AAACAGTCAT TAATTTAAGG TA  
 A/G  
 GAATATATCA TCCCTGAATA CAAAAGTAGG TATTTACGGG TCAAATGCAG AATATTCAGT  
 GAACAGTTTC C

01T418 132bp  
 CCTGTAGGGT CACCTGGAGC TGCAACAGGG AATTTTCTCT CCGTATACCT AACTG  
 A/G  
 CCAGAGCTTA AAACAATTCC AGATCTCCTG ATCTATTTGG CTGGATAACA TAAGAATGCT  
 ATTTTGGTGA AGGTGA

01T420 135bp  
 CTCAGAACG GGCAAACATA TAGAGTCAAA GCAGATTGGT GATTTGCTAA  
 G/A  
 GGCTGCAGGA AAAGAAGATA GGGATATTGG GGATGATGGC TAAGTGGCAT GGGGTTTCTT  
 TTTGAGGTAA TGAAAATGTT CTCA

01T421 123bp  
 AATTCTTCAA ATCACCTTGT CGAATTGGGT GAATTAAATA GGGTTCTGTC CCTAAACTGT  
 GGCTTCAGTC AG  
 A/G  
 TCTTATCTTC AGTCTTTTAG GTTCCCAAGG TTTGTGCAAG GGCTATCATG

01T424 124bp  
 GTCAAAAGAG GTCATTTTGG AACTTTAAGG TTTAATGAGT GCCCTATTAA ATTTT  
 G/A  
 GATTTGCATA GGACCTGTGG CCCCTTTGTT TTGGCCAATT TCCATTTGGA ATGGGTATAT  
 TTACCCAA

01T425 145bp  
 GCCTTGGTAA GAAAGGGATG GGAGACAAGG CTAGAATGGT AAACAGGGTT CAGACTACAG CTAC  
 C/T  
 CAGTGGTGGG TCTAGAAAAA TAATGACCCA CATAGAAAAG TTAAGTGAAC ATATGATCGA

Table III

GGAGTTTTCA TAAAATAACG

01T426 149bp  
 ATGCGTCTTC CCAAGGATAC GATGCACCCA CCTTCCTTCT GTCC  
 A/G  
 GTACCTCACC ACACCCCGTC TTACTCTGGG GCTTTTCTTT TCCTTGCAACT GAGAAGTAC  
 AGTTCTCTCA ATTTTATTTC AACTTGGGGG TTGTCACCAG TGTT

01T427 131bp  
 ACTTCCTGCT CATCATCAAA CAGCCCGCCA AATCCAAGTT AAAGGATCTC CATCCCAACA  
 TCCCTCTAGC TAGATCCTGA ATCCCC  
 C/T  
 GTGGCTACCC CTGTCCCATG TAGAGGGAAG TGTAAGTAAG GGAA

01T428 109bp  
 GGGTATATTC AGAGAGTCAT GGTAATGTT TCTTGCCACT AAGAGAC  
 C/T  
 GAAGACTGTC GTCTGATCTA TGCAAGAGAG AGCTTAATTA GGCATAGACT GGAGTCTGTT  
 T

01t429 93bp  
 ACCCACATTC ATTACCCAAC TCTTCATCTG AACCCCTGTGG TGTAGACA  
 T/C  
 GGGCTAGAAA GGCCAGAATC CAGTCTTTTG GAATGCATGT GGCA

01T430 149bp  
 TCAGTAGCAA ATATGAAGCT GTTACATACA GATACTGAAT AAAGGTTAAG TAAATCCTT  
 CACTCATTCA ACAAATATTT ATT  
 A/G  
 CTCTAAGCTT GGTGCTAGTA TATCAGACCT AAAATTTAGA GTGCCACCTT AACATCTTTG  
 AGCCG

01T431 121bp  
 TGTCTATTTT TGCTTACGTT GCCTATGATT TTGGTGTCAT ACCTAGGAAA CCATTGCCAA  
 AAGTAATATT TTTT  
 A/G  
 TATAGTTTCA CAACGGAATC CCACATGAGG AACAGAACAA TCAGTA

01T432 115bp  
 GAGGGGCATG GCCAGGAGAC AATGACAGCC CAGTGTGAGA CGTGCTTTAG TGTACACACT  
 TAGAAG  
 G/A  
 TACCAGAGAT GTGTAGAAGT AGAACTACCT AAATCTGCCT GGAGAAGG

01T433 142bp  
 TCTGTGCTAG ACATGGTGAT GGGCACTGCC AATTAAATCT GTATTATAGT TTAAAGCCTA  
 A/G  
 GAAGAAATTC TCAAATCCAT TTCACCTATC TTAAATCTTA GCAAACCAAC CATACTGTGT  
 CCGGATTGG TTCCTCCGG T

01T435 126bp  
 CCCCTTTGCT TGAATTCCTA GGCTTTTGTT CTATACTGAG AATCAGCCAG TGCTCCTTAG  
 GGGATATACC TTGAA  
 A/G  
 AATATCAACT CATCTGTCTG AGATTCCTTT GACTTCAGGA TCTTAACTCC  
 01T436 148bp

Table III

AATGACAATT TCATAGCTTG GGCTTTGATG GGTAACCTGC AGCCCCACTG GCC  
 G/A  
 CTCCAGCAGA TGGTGACCCT GTGGGTGGTA GAGAGGCTTG AAGGATCTAG TGCATCTCAG  
 CTGAAAGTGG CTTGTCTCAA ACAGATGTGA GAAG

01t437 142bp  
 TCTATCTCAA GGACTGAGTT CTTTCCTGGA AGCATAGCTA GGACTTTTGT TATAGAAGCA  
 AGTCAAGGAA GAGAAAAATT TTAAAGAG  
 C/T  
 AGATAAAGGA AATGGCCCTA GAAAAGTGAC TCCCAGGCC ACATCAAATA CTA

01T438 129bp  
 CCCTCGGTTG TCAGTTGCTG GTTTTGCACA CTGCGTCAGC TTCTCCC  
 A/G  
 TGTGCCTCTC TGGCTGGTGA GCCTTCATTC CCCCTGACT GGCTGCCCTG TCCCTCTCTT  
 ATTAAAGGAT GCCTTGGGCA C

01T440 145bp  
 TCTTTTTTGG TCTCCTTTCA TCACTGTGTG ATTTACTTTA ATAGTACCCT GTCAAACCTAG  
 ATGACTCAGT GGCCTCATCA  
 C/T  
 AGCTTACAGA GCATTTTCATC TGTGGTCATT CATCCTGCCT ATGAAGAAAT TGACATGTAG TCAC

01T441 149bp  
 GGTGGGGTCT TCCTATCTTA GACCCCTGTA TTATATAAAG GTACACAGTG CACCTCTTCA  
 TAACATTCAG TAGT  
 A/G  
 TGACTAATGA CTCACTGAGT CCCTGTTTTT CCCATAGAGT TCCAGGCTCC ATGGAGTTCC  
 AGGCTTCATG AGGG

01T443 140bp  
 ACTCAGGGTC CAGCTCTTAT GCTCCTGGAA CAGATTGTTC CAAGGTTGAA TTCAGACCGC  
 C/T  
 GCCATTTCTT TGCTCCAGGC TAATCTTAAA TGTTCACCT GGGACACTGC TTGCTCCAGC  
 ACCACTCTTT GCTTATACT

01T444 133bp  
 GTCAAGTTAT GCGGAAAATC CTATTAGAAG TATTTCTTGG TATT  
 A/G  
 GACTAGATTT GTAAGTTGAT TGGGTGCAGT TGAAATCTTT AAAAACCCT ATTAAATTTG  
 TGGATTTAAG CCCAAAAGAC CCTAAATA

01t445 145bp  
 TCCTACTGAA GTGGCACCGG ATTTTGCTGT TGGGGGAATG CAAAAGGGTC AGGCTTCTTC  
 ACTCTCTCCA TGA CT CAGGG GTGGTAGGAA CAGAGGCAG  
 C/T  
 GACTGCTGGG AATTGAACTC ACAGAAGAAA GCTGAATCAT GGCTC

01T446 144bp  
 GACATTTTAA AGGCAGCAAA TTCAAACTA TAACTCAGGA TAGACACTGA AACCATACTT  
 C/T  
 GCACCAGATT AAGAAACTG GCTGTTGGTA GTTATCAGTG AGATGGCTTC TTTTAGAAAA  
 TTGTTGGCAA TGAAAATAAT ACT

01T448 125bp  
 ACTTGAAAAA TGTATTTCAA ACCTGCATAT TTCTCTGCAT CTCCACAGCC ACCACGCTAT  
 TTAAGCC  
 G/A

Table III

CTGTTATCAT CACCTGGACC ACTGTGGTTT TCTCTGTTCC CTAACGCACC TCTTTTC

01T450

CTTACCAGCA CTTGATATTC TGCGCTCTCT CTCCCATTC AGCTGTTC

C/T

CTTTCTAACT GCTCTTGTCT CTCCCTTTC TTGCCTCTCCC GTTCCAGTCT CTCCAGCCTC

01T454

144bp

CTAGACTCAA CTGGCTGGGT CACCGATGGC CATTTCATCT GTGCGTAGCT ATAGGGATTT

AAATAGGAGG ATTTTGTGA AATGAAGACA ATTGACC

A/G

ACTGTGCGTG GAATCAATGT GCAGGATGAT TCACCAGGCT TTCTGC

01T455

147bp

CTCCTGACCT GAGGTGATCC GCTCACCTTG GCCTCCCAA GTGCTGGGAT TACAGGTGTG

AGCCACACCG CACC

C/T

GGCCAATAAT ACATTTTAGT TCAAGATTAG TGAGAGCTAA GGAGAAATGA GAATGCTGAT

TGTTCTGAAA TT

01T459

120bp

ACAAACAGAA GCTACATGAC AAGTTTTGCT CTGTTCAATT TTTCTCTTTA AACTCTACTG TGT

A/G

CTGTTTGGA AACGCTATTA TTTCAGAAGG GAGAATCTCA TCTGGAATCA GAAGAT

01T462

149bp

CTGCAAAGTA GATATTCTGA ACCCTCATTT TACATTTGTA GAAACTGTAG TACAATTAAG

TGATTTACCT TGGACCAC

C/T

TCACTATCAT TTGAATCCAA TTATATCTAG TTGCAAAGCC CACACTCTTT CCACTACATC

CTGGTAACTG

01T464

145bp

AGGTTAGAAA AGCAAACAAA GGTACAGTAT ATCTACAACA CCTTAAAATT GCCACTGAAG

TTTAGATTTA CAAGTCAC

G/A

GAGTTTCACT TAATTTCTGC CTGAATATGT GTGAACACTC TTGGGCCATG AATGCCGAAC

AAGGCT

01T465

137bp

TATTTGCAGT GTTTTCTGAC AAATATTTTT CCTCCAGATT TTAAGC

A/G

TGTTATGATG AGTCAACCTT TATGTTTGTA AAGCCTTAGT CTTGTTAATA ATGTATAACT

TCCAAATGAA TCATATACTT ATGCATAGCA

01T469

125bp

GCAGCAATTT TAGAACC GTT CTAATTTGAG CCAAGACATT GTCTTCATAT GCCCA

C/T

ATCTGCTAAT CAATGGATTC TGCATGCCGC TGGATGGAGC TATAACCTCC AGCAGGGCAG

CTGCCTTTT

01T470

115bp

ATTTGAAATT CACAAGTGTG GGTATCAAAT ACACATAGGT GCTCTTAACT CAAGGATAAT T

A/G

AAGCATGAGC TCAGGCTCAG AGAGGCTAAG AGATTTGTCC AAGATCACAT AGC

01T471

133bp

Table III

TTCTTCCTCT CTTTAGCGCC TCCCTCTCCC TCTGCTATTG CTTGCCATGT TGGAACTGTC  
AATCACGGGA TCCTCTCCCA CTTTCA

A/G

CAAGGGAGGG CAACTGACCC AAGCAAGGCC TCTCAGACTC CTCCTC

01T473 131bp

TTTTGAACCA CAGGCCTCAT AACTGAAAGT AGACTCACCT TTTTCAATAA TAGATGACAA  
AATGTCGGAA TGTTTGCTTC C

A/G

AATATTTTTTA TTTGGCATTATCCTGAATC ACTTAATATC CCTGTGATG

01T474 143bp

CTGCCACACC TCTGTAGCCC AGAAAGGAAA TTTTCATATT TACTTCTTTA GAGAAACCAA  
CTCCAGTCAT CTACAG

C/T

GCTTTCTTTC TTTCTGACCC TTGGAAAAA TGTTATTTGC CACGTTTTAG CTCATACTGC  
TGGCCT

01T475 14 bp

CTAGAGAGGG CCTGACAACG AAGCTGTTGT GTCAGGGAAA TGAACAAGCA GAATTGTTTT  
TTCATTGGGC

A/G

GGTAATGCAT TTATGTTTCCT GAGGGAATGG ATACATCTTT CCGTTTATTT TTTAAGCAAG  
TAAAACAAAC AAAACAA

01T477 107bp

CAGCCAGACC TGCCCTGACT ACAACCCCCA CACTTCTTTC CTGTGTGAGA AAG

C/T

AAGCCCTGGT TCTTTCCGTT TCTATAGCAA TGTTTTCTGT TACGCGTAGC CAA

01T478 143bp

GCTGGATGGG ACCAGAAAGT GAATACGCCG AGGCATAGGG TTGTAGCAGA GAAAGAGGTT  
TCATCGTAGG G

C/T

CACCGAAGGA GGAAATGGGA GGAAACGTCA AATCCATCTC CCTGAGGAGT TTGGGGCTGG  
GGTTTTTAAG G

01T479 106bp

AGAAGGGCGA GGAAGGACTC TTCCCTGGGG CCTTCAGAGG AAGCACAGCA C

G/A

GCCGACACCT TGATTTCAGA CTTGCAGTCT CCAGAACTAT GAGAATACAT TTTT

01T481 134bp

CCTGGGTCCA TGTGGATGGG CCTTGAGTTT GAGTCCATGG GGTTTAGCCT GGTGCT

A/G

GGGTGAGCCT GGAGCTTGAG TATGCAGAAA GAGACCTGGT TCTTGGGCCT GTGGGGACCT  
GTCTGGATCT TGGGTCC

01T482 147bp

GTTTCCCAGA AACTGTGAC TGTACTTTTA CCAGAAGAAA TATATTAGTG TAACAGATGT  
TGACTCTACT GTAGAAGCTG TGTG

C/T

TAAACCTAAC ACATGCCTAC CAAGTAAAG TAACTAGTTT TGCTGTTTTG TTTTCTCAGT  
GC

01T485 148bp

AGTCATGACC TAAATTAAAC AGCATATTCA ACTTAACAAA TTCCTCTATA AACTT

Table III



C/T

TATGGATCCA CTGAAAAATG GCCATCTGTT TCCTTTTATG AAGTCAAATC ACATCTAGAA  
 AATGGCACAC ATACCGTAAG TGTTCCCTCA TT

17D143 not use Bsl1

CTTCCTAACT CGGGGGGAGA ACGGGGCCAG GCCGCCCAGG GGCA

G/A

GAGCTTTAGA ATCAGGGTGA CCCCCACCCC TACTCCCCAA GCACAGTCAC

17D256 116bp

CTCCCAAATG GATATTCATT CACTGCATTC ATCTTACCTT TTCTGAATGC A

T/C

CACATTTAAA GCCGCACTAT GGGGAGCCAC GGATACATAG TCACTGTCAT TAATCATCGT CACC

17D279 108bp

TAGAGATGGA GTTTCACCGT GTTGCCCGAG CTGGTCTTGA ACTCCTGGGC TGAGGTGAT

C/T

TGCCAGCCTC GGCCTCCGCC TCCTTTTTGT CTTTACATCT TTTATCGC

17D350 142bp

GATCTAGCCT CTCTCCAAAC CCTTCTTTTG TTATAGAGTA TAAAATTCTA GAGTGAAAAC TAA

A/G

TTTCATGGCT CTGAAGACAT TTCCCTATTG TGTTTTTATT ATACTGTACT TGAAACTATT  
 GCCATTGTGT GATACATC

17D402 139bp

ACTCCAGCCC GGGTGACAAA GTGAGACCCT GTCTTAAAAA CAAAAAAGAA AAAAAAAGA  
 AACTTGTTGG CTCGATTTC A GTGTTCTTCA

A/G

ACTTTGGTTG GTTGACTGCA TGTACTATTG CGAGGGAAAA ACATTCCA

16\_001 125

CCTCAGTGCA GCTCCTGGCT TACCCTCTTA CTGTGGGGGA TTTACAGGCT  
 GGAG

A/G

TTGGGCCGGC ACCTTTCCAG AGCAGTCATC CCTCTGACAT GTTCAGGGAA  
 TTTGCCAGG TCTGCCATGG

16\_002 139

TGCTTTTTGT TTTCCCAAG TGTGCAGCTG GTGCTGAGAG GTGATGGTGC  
 TGCTTGTCCT CACACAGGAG GAGGAAGGTG AGGACGGCGA TCCATC

A/G

TCAGGGCCCC CAGGGCCGTG TCACAAGCTG CCTCCCGCCC CC

16\_003 106

AGGGTTGGGC AGTGAGACGC GGCTGGACCG CAGCAAAGGA GATGC

A/G

CGGAGCGACA CAGTTCTGCT CGACTCCTCG GCCACACTCA TCACCAATGA  
 GGGTAGGCTG

16\_004 127

GGGCCACTTA GGCGGGCAGA ACGCAGGGGC CAAGGAGCAC CACAGGAAGA  
 TCCCAGCCCC GCTGGCGATG G

G/A

CACCTGCGTG CAGGCAGAGG GCAGCACATG GAACAGCAAC ACAGGCCTGC A  
 ACAGG

16\_005 145

Table III

GTGCGTGTG ATGAGTGGGT CGCACCAGGG TGGAGCCTCC TAGAAGGGCA GGA  
C/T  
GCACCATCCT TGGGGAGTGG CCTGGAGAGG CCTCGGGAAG GGGGTCCAGG  
GTGGCTGAGC CTCAGCCATC ACCCATGCC GTCCAGCCCT

16\_006 108  
GCACAGCCCA GCAGGGGGTC CTGGGCCTCG TCTGCCAAGC CTGCTGCATG CCTGG  
A/G  
AGAGGGGTCA GCTCTTGGGA CTCTGGAATC TTGAGAAGGC TGATCCCTGG TG

16\_008 147  
GGATGGCTGC AAAGTGCAGA CCGTCTGTGC ACGAGGGATG TGAAGAACA  
TCTCCCCAA GTTCAGAGCC AGTTCACG  
G/A  
GTGCAGGCAC ACCCACGCAG AGCCCTGCCT CCCCTAAGGA GCCCCCGAG  
GTCAGCAGGG TCCAGGC

16\_010 115  
TGCGTTAACT TTTTCGCAGA CGGGAAACTG GGCAACAGGG AGGCTACAGG  
CCTTGCAGGA GGCCATCGGC  
A/G  
AGTCCGATGC TCAGAGCACA AACGCCTGGCC TAAGAGGTGG TGTC

16\_011 118  
AGGGTGGAA TCTCTGTAA GTCCACCCTG CCCCAGGGTG CTCCTACCCT  
CTTGGTCTTT TTAAAG  
C/T  
CAAGGTGCGA TTTGGGCACC TGA CTGTCCA GTTTACCTTA ACAAGTTTGG  
GA

16\_012 145  
GTCTGAGTCT CGAGTATGTG ATTGGCCAGC ATCTTGGGGA CGGTGGTG  
A/G  
AGGAGAAGCA GATGTCCACA AAAGACAGGT TGCTGAGGAA GAAGTACATG  
GGGGTGTGCA GGCAGGAGTC TATGCTTACG GACAGGATGA TGAGCA

16\_013 96  
CCCTTCTCCT CCCAGCCGGA CCAGACTCTG CGCACCAGG TGTGGGCT  
C/T  
CCTCTGTGCC GGGGTGTCTC CACTCGACTC TGTTGATGTT TGGGATG

16\_014 135  
ACATTCTGTG GACTTGGACA AATGTATAAT GATGTGCATC ATT  
A/G  
TAGTGTGATG CAGAGTATTT TCACTGCCCT AAAAGCCGTC TGTGTTTCAC  
CTCTTCATCC CTCTCTCCTT CCCAAAACCC TGGCAACCAC T

16\_016 149  
CATCACCTTC CAGAGCTGGA GGGGACGGCC ACCCATACCA AGGTCCTTTA  
GCTGACACCT AAATCAGGA GCTAACCATG TG  
C/T  
AGGTCACACA GGCCGAATCA CAGCAGTGAT GAGACGCTGG GGTCTCCACA  
CAGGAACCCA ACTGAC

16\_017 123  
AAACCAAGA CAGCTGAAGC GGGCTGTGCG TTTGTCCCC AGCTAGGCCC  
AGGGAGTGG CATCTGG

Table III

A/G

ACGCAGGATC TCCTGTCCTC CCGACACCTC ATTACCCATA TATGGGCACC  
AGCCT.

16\_018 115  
TAATCCAAAC AAACCTAGAGG CTAATTGCCA TTCCCCAGCA CAAAGCTGCA  
GTGACGATGA TTCTTTAATT C  
C/T  
TTCTACGTGC TCACAGCCCCA CGGCGCTCTA CTCTGCTCAC TAA

16\_020 117  
TACCTGCACC AGCCCATTTCT AGACCTGGCT CTCTTTCCAG GCCAGG  
C/T  
GGGAGCTCCC GAGAGGGGTC TAGGCATCCC TGAAGTCCAG GCCTGTACTA  
TTAAGCAGCT CATCCTGGTT

16\_021 132  
TCAGAGAAGC CTTATGCCGC TCGATTTCCC ACCAGCTCTG GAGTCGGGTC  
CTCTCCACTT CCACACATTC  
A/G  
TTTCCACAAG ACAGGTCACC TTTCCACCAG TGTGGACGTC TCACAGTAGA  
ATCAAGGACA A

16\_022 98  
GGAATGCATG TTTCCCCAAA CATGTACTCT CGGAGGTCAT ATTAGTCT  
C/T  
TTGCTTCCCT GCTCTTTTGT GACAAGCAAT GTTAGGATAG CAGTGGATG

16\_023 128  
TCTCTCCTTC TGACTTCTGC GATGGGCCGG GGAATTTGGT TTACATAAGC  
AGCCCCGTTT CTCAGACCCT  
C/T  
TGTATCTTCT TCTGGAGTAT ATGAAGGCTG TGGTACCAGG CCAAATTTTG  
CACACAA

16\_024 121  
AGCCGGGTCC CTTCTCATC AGTCACCATT TAATGGAGAC TGAATGGTTG TGGATAC  
C/T  
TTTGTTAGGG TCATCAAGAA GGTTTGCCAT GCTTGGCTTG GTAAGGAGGA  
GGTTGTGTGC TCC

16\_025 89  
ATCTTGTCTT CCTGTCACAC CCACCTGGCA CCACCTTCCA CCCAGCT  
C/T  
TGAGTCAATC CACCACTTCC TCACCTGTCA ACCACCAAGC CTCATTAC

16\_026 105  
TCTCCACATT AGGGCAAAGT GAGCTCACAT CTCTCTTACC TGCTCTCTGG  
GCCTCCC  
A/G  
GCCTGGACTC GCACAAGGGC ACCATCCCAC TACCCCTCAT ACTTCCA

16\_028 92  
TGCCCCACGG GCCTTACCTA GTCCCCGAGA ACTTCCGGGA GAG  
A/G  
AACCTTCAGC TCATCCAGTC CATCAGGGAC TTCCTGCAGA GCGACGAG

Table III

16\_031 136  
TCCCCTCCTA ATGTGTCAAT GGCTTTGCCA GGAATTGCAT CGGTGGTGTG TCAGG  
C/T  
GGGCTGTTGT CTGGTTTCTG TGACAGAGAC CCTGAGCAAC ACTGGTTTAG  
ACAAGGTAGA ATTTTCTTTC TTCCCACTTG

16\_032 149  
TGAGGCAGTT CTGTGAAATC CTCTGCATGG GCTTTTGAAA TTCCAAGGT  
CTCTTCTTAA GGGCAGG  
C/T  
TGCACAGTAA TTTCCCGAGG AAGGCTTTGT TCCATAAACC CAGGCCTTAC  
AAACAACAGT TTCCGCCTCT GATATGTATA A

16\_033 141  
GCATTACTCT AGAATTGGCA TCAACCCCAA GCAAGGGAGC AGGGCTTTCA  
TTCTTATGTG CCTA  
C/T  
GAGTCGAGTC ATTCACCAA GAGATGGAAA CTTCTAGCTA CTCTGGCTCA  
TTGCATGTTG AGGGAAAATT TCTCCA

16\_035 120  
CACGCTCAAC AGCTGTTCCC CTAGCTGTAT CAAGTCCAGG CCAGTGAGCT  
TGCTTCTCTC C  
A/G  
GCTTGTCTCA GCAATTTTGT TTTCCCCAC TGCACAAGTT CCTAACAGCT  
CCAACGAG

16\_037 147  
ATGGGCGCAT GGGCTCTTTT ACAAATGTGC CGTGGTCCGT GCATTGTGCT  
GCTGTTGTGC CCTCTGCTG CAA  
C/T  
GGCAAGGAAG TCCCTTTGCC TTGCGTACAT GGAAGTTGGG TGCCAGGCTC  
CCAAAGCAGT TCTTCTTGTG CCC

16\_038 127  
ACTCCCCCAA ATCTGGGTTC GAATCCCAGC TCCACCACTG CAAGTCTGGT  
TGCTCTGGA  
T/C  
CAGTTACTTA ACGTTCTCTA AATGTCAGTT ACATCCGTGA GATAAGCTAC  
CTCGCGGGAC TTCATT

16\_039 111  
TTGCCCCTCT GGAGTTTACA GTTCGGGGGC AGAGACAATG AATAATGAG  
A/G  
CAGATAAGTA AATAAGGTT TCAGATAATA-CTAAGGGCAA TGAAGAAAAT  
AGTACAGGTG A

16\_040 143  
CATCTACAGG GTTCCTTCGG GCTATGTTTC TAGGGTGAAT GGCTGAGATA  
TAAGTGATGT GCTAT  
C/T  
CAAGGCCTTT GATCGGTAGT GGGGGAGACT CGGGGCAGGA GATGTTTTTG  
GCGTACCCTG AGACACCATC ACATCAT

16\_041  
GGGTTGCCGT TCTAATTAAT CTCTTATCAG TGCAGTCAGG GGTCTCCTTT

Table III

GGAGCCTCTT GTGGGGGTCC CACTTCAGTA GTTACTAGAG CAGCTTT  
 C/T  
 TGTTACAGAG GTCCCCTTTT GAGTAGGTTT ATAAGGAATG TGAGAATT  
  
 16\_043 124  
 CACACTGAGG CAGCACCTCC GGGGAAGTCT CCGTGCTCCG ATGCTGTGGC C  
 A/G  
 TGTACAGCAT ATGCAGTCCC CAAAGGGATA TTTCAGCACA GAGTTTCAAT  
 GTAAAATGAC ACACGCTACT GC  
  
 16\_044 135  
 GCATAATCCT TAGCACTTGA AGACTTTTTTC AGCACCAAGG ACAGCAAAAC  
 GTCATCGTAA TCAGCACCCA  
 C/T  
 AAGCATCCAC CTTAGGATTG CCTAGGGGCC GGCCGCTCTC ATAAATACAT  
 AAAGGGGAGG AAGG  
  
 16\_045 138  
 AGGGCGGCCT CTCCTGCAGC ACGAGGCCTA CCTGAGGGGC AGTAGGAGGA  
 TGAGTTGGGC ATTCTCC  
 A/G  
 CGAGAAGCTC TTGACCACCA GGCTCTGGCC CCACTGCTTG CGCCGCCACG  
 CCGTGCGGCA CTTGGAGTCG  
  
 16\_046 137  
 TCCAGCTAC TTGGGAGGCT AAGACAGGAG AATCGCTTGA ACCTGGGAGA C  
 A/G  
 GAGTTTGCAG TGAGCCGAGA GTGCGCCATT GCACTCCAGC CTGGGCAACA  
 AGAGTGAAC TCCATCTCGA AATTAAAAA AGAGT  
  
 16\_047 106  
 GGTGAGGAGC CTGGAGCCCC ACGCTGGGCC CGAAGGTTCA AGGGCTTCTC ATCAG  
 C/T  
 GGCTTCTCAT CCGTCTCACC CTGGTCTGCG GCTTCTTCTC TAAATGCATT  
  
 16\_048 111  
 AGCTACTGGA TGCACTGGGT CCGCCAATCT CCAGGGAAGG GGCTGGTGTG  
 A/G  
 GTCTCACGTA TTAATAGTGA TGGGAGTAGC ACAAGCTACG CAGACTCCAT  
 GAAGGGCCAA  
  
 16\_050 133  
 ATCAATTTGC TGCTGTTTAG TAAGGTATAA ACTACAGTTA AGGTAAAGA  
 CCTTGCCACA TTCTTCCAT TTA  
 C/T  
 AGGGTTTCTC TTCGGTAGGA ATGATCTGAT GTTGAGTAAG GTGCAAATA  
 TGGTTTAAG  
  
 16\_051 145  
 TGATCTCTCC AAGGACTGGC CTGGAAGGGA CAGAGAAATG CGAATGCCCT  
 TT  
 A/G  
 AAATACTCA CAGCGTATAG TTGAGTGGTT TCCAAAGACC CCCTCTATGC  
 TGCCAAGCCC TAAGCATGCT CTCGTATCTG TTGTTGGGAG AT  
  
 16\_052 98  
 AAATACTGAG .GGGTTGGCAT GAAAGACCCC CACACCCTGC TGCCTGCTGC

Table III

A/G

GGAATTGACC AGGGCATAGG CTTAGAGGGG CCTCATCAAT AATAACC

16\_053 125

CTCTCCCCAC TAGGACAGGC ACGTGTCTC ACTAGGACAG GCACGTGTC

T/C

TCATTGTGTG TAGGTCAACA TGGAACCTTC TCCTACTGCT TGCTTTGGTA

AGAATGATGG GTTATCGGGA GGCTG

16\_054 116

CATCTTGATG CACCAGGGTG GTCCTAATGT TCTCAGATAC ATTAGAATCA CACAAT

A/G

TGGTCCCTAA ATGAGAGCCA ATTCTGTCTT GTCATCAACC AGAGAAACAG

CAACTTGT

16\_055 113

CCTTGACGTT CCCAGAGATG GTTAGGGAAG AGGGACTCCC AGTCAGCAAC A

A/G

TGCGATCTTG TAGTAAATGC CAGTCTCAGC TCCAGGTTTG GTTTGACCCC

ACATGTGTTG G

16\_056 131

TGAGGGTTCT GTGCTTTTCT TGCTCCAATG CTGAAGAATG GCCTGCTGCT

TTCCCAGGTG TCACGGGCAC TGAGAAAGGG CCCC

G/A

TGGCACCAGG AGCTAATCCT CAGGGGTCAG AGGCTGTGGG AGATTC

16\_057 139

CTGGGCTCCA TCCTCCCTCT GGCCTCACCT CCCCAGCCAG CCCAGG

C/T

TGCGCCAGCA TCTTCTTCCT CGTCCACACC CTGCCCTGCC ACTTCGCTCT

CCTTCTCTCT TGGTCCCTGC CCCGTTTCTA GCATGCCCC TT

16\_058 143

CTTAGCCTCA GAGGTGTGCA TCTACTCACA GAAGGGCTCA GTGGCTTCCA

GTGTTCAAGG TTAGTGATT GCACA

G/A

GAGCTGTTAT AGGACAAGCC CCGTGGATAC TGGTGGCTCA GAGGTCTTAC

AGATGAGGTT TCACTGG

16\_059 138

GCTTTCTGTG TGA TAGTCT TCTAACTGCT GTATAGACCT CCAGGCTTTG CCT

C/T

TCCATCCTGC CAGTGACACC AGGACTGCTG CCACCATTCA TGCTGTGCGG

ATCATTATCA TCCATGTCAC CTTTAGGGCC CACT

16\_060 117

CGGCCAAACT TAAATTTTAA AAAGAGGAAC AGAAGTCAGC CAGACCAACA

AAAGAGCGAC

C/T

GGTGTTCCAA GCATAGGAAA CAGAGGAAAC AGAGGCCAAA ACCTCGGGAC

TGTGGA

16\_061 125

GAGCCAATGG CCAAGAAACA GTTAATAAAA TAACAGACGA TGGTCCTGGC

CTCTACTGTG AGTGAGTAAA G

A/G

Table III

- 38 -

GCTTGCCCTG CAGAGATTCA GTGATCTGGC GGGGGTTGCT GAGCTATGAG  
GAA

16\_062 100  
ACTTCTTTT CTTGTCCCTC TCATCTAGGC ATGGCCATGC CTCTTCAT  
C/T  
GACTCCTGTG TGTCCCCTCC CCATTCTTGC TGTCAGACAG CGTGCTGGTT  
C

16\_063 140  
ACTTACAAGT CTGGGGTCCG GGGCTCCCCG GAGCTGGAAG ACCAAGGCCC  
CTGTGCCTGG GATCGCTGGG TTA  
G/A  
GGGCGGGTTA ACCTAGGGGT CCCAGCCTCC AAGTCTGGGG AGGATCCGGG  
TTCACGGGGT CGGAGT

16\_064 119  
ATAAGTGAAT TCCGCTACGA TGGCCAACCT CTGCCAAACC CAACCTGACC  
AGTGGCCAAC CTGAGCATCA CG  
G/A  
TGTTTCAGCCC ACTGATGGCT GCCTCCAGAT GCTCCCTGAA GGGACA

16\_065 141  
TTCTCTGCTA AAATATTGCC GTCTCAGTGA ATCAGCTCTA GATGAACTCA  
TTGGGTGATT GTAGGAGAAG CCCCTCCCTT TGGGGCTTGG AGAACC  
C/T  
TGGAAGGAG AAAGGACAGG TGGTGGGGAG AGGTGGGTTT CCCT

16\_066 112  
GTGACTGTTC CAGAAGCTGC CTACTCTTCT AGTGCCTGCA GCAATC  
C/T  
GAGGTGTGGA GGGCACTCCC ATTTCCCTTC CCTGTGCTTG AGAATCTGTA  
GAAATTGTGC AACTT

16\_067 119  
CCACTCTTTC CTCTGGCTTC AAGTCACAGT GTGCCAGCAT CCACATGGGT  
AACTCAGGGA TGATG  
A/G  
AGCTGGTCCC TGACAGGGCC TCACACCTCT CGCTGGTGGG CACTGACCTA  
TCC

16\_068 123  
ACCAGCTTTT CCCCAGGGG TTAGCCCAGG GCCTTTCCGG CACCCAGAT  
C/T  
GCATCTTCTT AGCTGTGCCC CAGAGAATGA GGTCGAGATT GTGATCTGAA  
~~ATATTTTCAA-GGCAGGTGCT-GCT~~

16\_069 113  
CCAATAGCAC TGTGCTTGAA TATTAGATCA AGAAATGGCC TGACAGCCCA  
AGACCCCTTC TCA  
A/G  
TGAAATTAGC TTGAGACTTC TGACAAGAAC GAAAGTATTC TGCCCAATG

16\_070 106  
CCTCCAAGCC TCTGCACCTT CTGTTTCTTG TGCTCAGGCT TCCCTCCACC  
TCCACCC  
C/T

Table III

TTTGTCTCA TGGTTGATGC TTCTTCTCCT ATGCCATGTA TTCCATG

16\_071 115  
ACACTCATAT CCACCTTTAT CCTAAGTCCC CAGACCTAAC TAATGCCTTC  
TCAGT  
G/A  
TCACCCAAAG CCTAGGTCTT CCCTTATTCC ATGGGATAAC TGCACACAAA  
ACCAGGATC

16\_072 122  
ACATGTTTCC TCTCCCACTT AGTTGGGGCC AGGCCCTGGG GAAGAGAGTT  
TGCAAGAGGC CCAGGTTTAG  
C/T  
TGAACACGTG GAACCATTGG TGAGCTCCTA GCTCCTGCAG TCCTCTTTCC  
A

16\_073 138  
ACTGCAGCTG CAGAATGACA GAGGCCATGT CCAAATCCC TTAGAGACAC TG  
C/T  
TGTCTTAGAG TTGTTAAAT AAGAGCCCC ATATCAGGTT TAGAAAATAC  
TGTCACCGAA CGAACGTCGC TGCTCTCAGC TCCAC  
16\_075 100  
TTTAAAGCCA CTGAGTTTGT GGTAATCTGA GGACCCTGGT GTATG  
A/G  
CAGATGCAAT TGACAGCAAT AACAACTTAA GCATACCCTG TATGGCAGAC  
ACAC

16\_076 143  
TGACTCGGGC TGGGTGTGGA TTCTCACCCC AGGCCTCTGC CTGCTTTCTC  
AGACCCTCAT CTGTCACCC  
C/T  
CACGCTGAAC CCAGCTGCCA CCCCCAGAAG CCCATCAGAC TGCCCCCAGC  
ACACGGAATG GATTTCTGAG AAA

16\_077 146  
CTTGGGGGAA GGTGTCATGA TTGAACACAG AACTTAGATC TGAGCTTCCT  
GGCAGC  
C/T  
GATGGAAAAA GGCAAATCA GTGAGCGCAT GGCTCACATT CACTCCTAAA  
AGGCAGCACA GATGAGATCG TAAGGCAAAT GGCTCTGCA

16\_079 145  
TATGAAGATG AAATCAGCGA TTCCAAAGCA CAGCTAGCTG CCATCACCTT  
GATCATTGGC ACTTTTGAAA GGATGAAGTG CTTAGTGAA GAGAATCA  
C/T  
GAACCTCTGA GGAATCAGTG TGCCCTTGCT GCATCCAAAC TTCTAA

16\_080 145  
ATCAAAAGCC CATAGCAAAT TCTGTTCTGT TCTTGGGGAA GCTGACAGTC  
TGATTTGGAG GCAGAGGACC CCAAATACAG GCAGCCTTCA CC  
A/G  
ACCCTGACTC AGGCAGTGAT ACTGCTGATG AATCTGTGGT TCCTGCCGGG  
AG

16\_081 121  
AGCGTCTAGC ACCTGGTACA AACCAGTGGC ATCTCCCAGG CATTTCTGAA  
CCATTTTCAC.

Table III



A/G  
TGCCTCTACT CTCCGGCCGT CTCCACACCA CCCTGTGTTC TGCCAAAGGG  
AGCTAAAATG

16\_082 144  
AAATTCAGGG TTTTCACAAA CGTAGTGAAT TTTCAGCTTG TAATTTGCTG  
TCTCCGGTGA GCG  
C/T  
GGTGCTGAGA AGACCCGTGA TGCTCTCTTT GAAGCCCATT TGCGGCATGC  
CCCAGGCCTG GGACCTCCAT TAAGCACCAG

16\_085 131  
AGGAATTCAG AGCTGAAAAAT GACAGGAGAG CTCCTCTGGC CATTTTACGG  
ATGAA  
A/G  
CTAGAAAGAG CAAGATATTG TCCAATCTTA CAGGGGAAAT GAGCAGAGCC  
AGGAATCTCA GGCTTGAGC TGGGC

16\_086 149  
TTGAGCCTGG GGGGTCCCCT CGCCAGCACA AGCGCCGGTT GGCAGCAGGG  
CTGGGGCTTT CCCTGAGGAA GGGGAGGAGG TAGCCCTGCA TGTGAC  
A/G  
GCGTGGGACA GTCCAGGCTG CACCTCCTCT CTCCAAGAGT GTGTCTGCAG  
GT

16\_087 145  
GCAAGGGAAA AGATGTATCA ATTTTCTCTA TAAATGAAGA GGCTGTTGCA  
TGGATCTGAG AAAGCCATGG GGTGAAAGGG GACAGGCCTC C  
C/T  
TAATGTTGAG TGACAGAGAG AACTGCAGTG GTAATCGTTA ACCAAACCAC  
CTG

16\_088 149  
AGTCCGAGGG ATGTAGGTGA CAGGGAGGCT GCTCAGCTCA GCCCTGCCTG  
CCTGC  
A/G  
CCACCCAGGC TCCCCAGGG AGGTCCAATC TCCCACCCAA GGCAGGACAA  
GGCAGACGAG AGCCTCACGA CACCGACAGT GACGCACACT TCC

16\_089 139  
CATGACACTG AGTGAGGGGC CCCTTAAGGG CTATGGGTAC AGGTAGG  
A/G  
ATGCTAGTTG TGGCGAAGAA AGCTAGAGCT GATTAATTAT GCAGGCAGCC  
CCACCTCTGC AAACCACCCA TCTGGGAGGT CAGCCTGCAA A

16\_090 124  
GGATGGGGGA GGTGGCCCTT AATTCTGCCT TGAGAAACCC CGCCTGAGGC  
CTCAGCACCT CTTGTCCAG CCACCCACA  
A/G  
GTGAGGGTCA ACTCAAGTGC CTGAGTGTCC TCTCTGCACC CTGA

16\_091 136  
TTTGGGGCAG CCAACCTGGC ACAGCTAATC AAAGACTGAC ATGGAAGCCA  
CTCCCTCTCC CCTCCCCTGT ATCACTGACA CCATTTTCC  
A/G  
TCGTCTTGTC ATCGCAGACT TTACAGTTGT TGTCAAGAGT CTAATC

Table III

16\_092 108  
 GTTCATGTGT CAATTACCTG GTTACTTAGT AACCAAGTAA TCCAGTAACC  
 AAGAAGTCAA GCC  
 A/G  
 TAGATTAAAT AGTCCCCAAC CGGGCAATAA AAAGGTCCCT GAGTACAAAT  
 TTGC

16\_093 85  
 CTACAACCCT CAAATTCAAG TGACAGAGCT GGGATTTTGC AC  
 A/G  
 TGCACATCCA TCAGTTATTG AATAAGGCTG CTCTGAAAAG GG

16\_094 149  
 ATCCAAGAAA TTAGACACAG CCCTAAGAGA AACATGCAGA AATGAGCAGA  
 ATAGACCCCA AATAGATCAA AATTCTGTCC CACCCTCTGC C  
 A/G  
 TCCCTCTCAG AATGGAAAGT CAACAGCAAA ATTAAGTTTG GTGGTGAAAA  
 AATAACT

16\_095 119  
 AAGGGAAAGG AAGAACATAT GGGGAAGGCC AGAGTGGAGA CAGGCAAACC  
 AGAGCCTGAA AACGAAGC  
 A/G  
 TCCTCTAGGT TAAGTTGAGA GTGTAACTT TAATCAGAAG GCAACAGAAC

16\_096 137  
 TGCTTCCAG CCTGGGCTCA GGTGACTCAA GGGAGAAAGC ACCT  
 C/T  
 CCTCTCCCCG CCAGGGAGGT CTCGCCATGT TTTGGAATCA GTACCATTCC  
 CTTGGGGCTG GGGGGCAGCC CCCATCTCTG GACCTGGCTG GA

16\_097 126  
 AAGTTGTAGA TGGCCAGCTG GTACCATGGA GTCTAATGAT GCCTCATCTG  
 TCCAGTGCTG ATCTTCGACA TTCCC  
 A/G  
 TGTCTGGGAT GGGAAATCCA TTTTGTAGAA CGAAAGGAGA CAGAAGGCAA

16\_098 130  
 AGATGTGTGG TCATTATCAC ACCGTTTGGT TTAATATTTA GCCAATGTCT  
 TGGTCAGGA GCCTCGTACA ATGGCTCTCC ACAATCCA  
 A/G  
 CACTACGATG ACATGTCTTT CTAACCTTCC AAACCACACT G

16\_099 137  
 GGAGAAAGAA AAAAAAACC TCAATTTCCC AGTGAGCTCA CTGCTTGCCT  
 CTCTTTCGAA GTTCCAAATT GCCT  
 C/T  
 CACTTTCTCA GAATTCCAAT CAGGGCTCCT TCAGAGGAAG CAATTTCTGC  
 CAGCACATGG TC

16\_100 148  
 ATTTAGGATT CCTTTGTTCT TGGAAAAGAC AGTGGCCTGA TTTTAGGAGC  
 A/G  
 GCATTTCTG CTGCCCAGCC TGCCATTTCT ATCACAATGG TAGTCAGTGA  
 GGGTGAATGT AACATTGCCG TGACTGTGAA CAGGAGGTAG CCCCATG

16\_101 133

Table III

CACAGGTTTT GCCTGTTTTG CTCTCAGATG TGCTCTAGCT CATAAGACAG C  
A/G  
TCAGGCATAC AGTAGATGCT CAGTAAATAG TTGCCAGTTG TGTGAATGTA  
GAACCATACA TCACCACAAT GCTGTACTAA T

16\_102 133  
GCTGTGTCTG CCGAGCCCAG CGTCCTCACA CAGCCCTGCT GCCACCCAGC CA  
C/T  
GCTGGCCCAC ACGTCCCTTA GACAGCCGGC CACCTCCCGT CCCACCCCTG  
CTGCTTGTTT TGTGCCCTCA CAGGTTTGCA

16\_103 144  
CACTCCTGGA TTTATGTGAC TCCCTTAGCT ATACTTTCCC AGCCCCCTGG  
GATGTTCCCC ACTCATCCTA TTCAC  
T/C  
CACAAAGAAA TATTGTCAAA ATCAATTGGG TGATGATTAG GAGCCATTAT  
CTGCCTGCTG TGCTGAAA

16\_104 139  
CACCTTGCTC TCATCTTTTT ACTCCTTTAA TGCTGACCTC TGCCAAATTG  
AATGAT  
A/G  
TATTTTCACA TCCTGACAAA AGGAACTGAC CATAGCTGAT AGAGCCCCAC  
ACCTCCTTAA AGAAAATGTT TTGTGAAAGC TA

16\_105 128  
ATGAAAGCTG GGTGGTCTTT GGGTAAGGAC AGGGGAACTA GGAGGTAGGG  
TGCAGGGTAA TGATTTGCTA CCC  
C/T  
TCTTTCTGGT AATACCACCA CCCTCCCTTC CTAGTTTCTT AGGAGGCCCT  
TGAT

16\_106 100  
TCTCCTGGGG AAGAAGGAAA CTAACCTCTT CCTATCCCC TATTTAATGC T  
A/G  
GCATCTGCTG TCCTCTGCTG TGGTAAACAGG GAACTATCTC CCAAGGAG

16\_107 141  
TGTGGGGCAG CTGGAATCGG GCAGACCTGA GTGTAAACTC AAGTTGGCCA  
CTGC  
C/T  
GGCTGTGCTG CTTCAGGCGA TTCTGTTGAC CTTTCTGTGC TACATAATGA  
AAATTCTTAT TTTACTGAGT GCAGGGGCTG GCGGG

16\_108 107  
GCCTCAATGA ACGACATCAG CGCTTCTCTA GTTGGTGAGA AGGCCCAGGA  
AAGCTTGGTC TG  
T/C  
GTCATACACT CAATAGCTTC TCCTACCCAG CCACCTACCC TGCC

16\_109 137  
TACTTGCTG GCTGCTCATG GTTAACAGAA GCCCAGGGAG AAGCTGACTC TA  
C/T  
CTTCTCTTCA GCCACACCCA AGATATTGGT ATAAGGGAGG CTGGCACCAT  
GAGTATTAGT ATAAGGGAGG CTTCCGGGTT GTGC

16\_110 142

Table III

GAACCCTATT GTGAAGTGTG CACGCAAGGG AACTAGGCTG TGCTCCTTA  
C/T  
GAGAATCGAA TGCCTGATGA TGGGAGGTGG AGCTGAGTTG CTGATGCTAG  
TGCTGAGAGT GGCTGCAAAT ACGGATTAAC ATTAGCAGAG AG

16\_111 121  
CTACTGGGTT TACATTGGAG ACCGTCCCAT TTAATTTCCA GGGTG  
A/G  
TGGGACAAAA TGGGCTCAGT TCTTACATAG CACACTACAC ATGTTTTAAA  
ATACAAAAC TACATTGTTG CTCCC

16\_112 109  
TCATCATGGT GATGGCATGC ACCTTTTTCA GGGCCGGAGC CAGTTCTTGG  
AGGAGACTCT GC  
A/G  
CAGGGCATGG ATCACTGTGG TGCCCTTTTC CTGTGCCTGT GCCTTC

16\_113 108  
TTTACATTCT CTACCCTGTC ACACAATATT TCACAAGGGA ACCTGGACAA  
AGGGAAT  
C/T  
GGTGGCAGAA GGATGCTACC CTTGCCTCTT ATGAGCTCCC ATTCACTTCA

16\_114 139  
GTCTCCTCAG TGACCATAAT GCTGAACAGT TGAGTTTTCT CATTGTCCCC  
TATTA  
C/T  
ATCCTTCACC TCACAACTCT GTGGGAAGAG CAGCTGCAGG GTGCACTGAA  
TATTAATCTC AAAGCAGCAG GCTGATCAGG GAA

16\_115 128  
TGAAAGTCTT TCCTGGGTGT CCTATAATGC AGAGAGCCAA AATGATCCTG  
AAGAAGT  
A/G  
TCTGTCCCCA TGCCTCATCC ATAGCATCTG CCAGGCCTCA CTGAACCAGC  
AGAATCTAGA CCTCAGTCTT

16\_116 129  
ACCCACTGCG TTCTGTTTTT TAGTCATCTA ACATACTTTG CAGACTTCTA  
GTCCCATCGA TACAGAA  
A/G

GGAGTCTACA AAAGAGTAAA TGTGAACCTG AGAGAAAAGT GTCCCCATCT  
GGCACAGATA A

16\_117 123  
CAGCTAGACA CCATAACCTG GCTCACTGTC TGGCCTTCAA GTTTCACTCA  
GCAGA  
C/T  
AAATGCACCC TTAAGTAACC TGGTAGGGAA CCTGTCACTC TACATAAAGA  
ATGTATGGCA TGCCACA

16\_118 141  
ATCGGCGGTG CTGAGCCGTG AGGTCCCCTA CCTGCCCTGT CAGGCAAAT  
A/G  
CTTGTGTCAG CATACTTCTT TCATCCGTCA CTCAGCCAGA GTCTGTAAGA  
CAGACTCAGC ACTAGGTCAC ATTTTGAAAG AGAAAATAGA

16\_119 105

Table III

GAAGATTTTT CTTCTCCTC CCCCTGTGAC CAATAGCCAA AGACATATTT  
TGGGATG

C/T

ATTAGTGCAC TGGGACCTTA CTCAGTCTAT AGATGACCAA GTTCACA

16\_120 133  
AAAGGAGAAA TACCAGTATC CGTCTTAAGA GCTGCTCTGA CAGCAACTCA  
CAGTTCTGAT AAACACTATT TAAGTGCCTT GTGAA

A/G

GCCTTTTTTG GGGAGGCTGT CAGCGAAGCA AGTGAGACCA TGTGATG

16\_121 145  
CAGTAAATCC AGGGCAGATG TATGAGGTAA TGAAAGAAAA TTTAAGAATG  
CACTCACACA TTGATGTGAG AACTATTAAAG ATCCCCTTCT CTCTCT

T/C

CTATACCTCA AGTTCGTTAT CATGCACTCC AAGCTACCAA ATATTCCA

16\_122 141  
CGGGGACAAA TTATTCACCA ATCTTCATCC CAGGCTCAGA GGAAGATTAT A  
T/C

ATCCAAGTTT TCCACTATAA TTAGGTTGGA GCCATATGAC TAGGCTCTGG  
ACAAAAGGAC AGTGGAAATA CTAGGCATCA CTTTTAGGC

16\_123 130  
TAGACAAAAG GATGAGATCT TGGTGTGGGG GGTAAAGGA TGAAGCTTTT  
TCGATTCTTC TAGCATC

A/G

TGCTAGACAA ATTCCAGAAA CAAACTGGAT GCTTATGATG GAAGCAGCAG  
AGGCAAAGA GG

16\_124 127  
GCTGGAATTA CACTGTGATG AACTAGGTTC CCACACTATT TGGTGGGAGT  
GAATGAGAGG CTTTGGATGT GAATGT

A/G

GGTGTGCCTT GTTCACCTTG CTCAGGTTCC AGCAGGTGCT CAATAAATGT

16\_125 119  
CTCAAGTGCA CATGAAAACC TTAAAGTCAT TACAGAATTG CTAGTCCACA T  
T/C  
TAGCCTCACA GTTAAATTTA ATAGTTCATT TGTGAAATTA ACAGACGAAT  
TTGTCTCGCC TGCTAGA

16\_126 105  
ATACCATAGC CACCCCCGAC ACCACCACCA GATTTCCAAG ACCCCGGACC  
CAGCACCC

T/C

GAAGGGTCTC TGATTCTGCA CTGGAGCAGT TTCTTCTCCC AGGCCC

16\_127 136  
CTACTGAATC AGAAACTCTG GCAGTGGATT TCAGTCCTCC AGGTGACTCT  
AATGCAC

A/G

CTCAGGTTTG AGAAAGGATC CCTGCCCTA ATCCATCAAG CCAGGCCAGG  
AGAGTGCAAT CGTAGAGTCC ATGTGTCC

16\_128 139  
GTTGTTGTG TCTGGTACTC ACTCTGTGTG CTGCATCTCA CTTTCATCAT

Table III

C/T  
 ATGACAAGGT GTGCAGACAA GGAAGAATGT TCCTCTGGGC TGCTTACTGA  
 TAAGAATCAC ACAGTGTAAG CCTTCAAGG GAACTTAGA

16\_129 131  
 TTGCTATCAT GTAGCTAGAG TCGATTAAGT GGCCAAGGGT CCAAGAGACA  
 GGTGAGACCA TGAGGAGGCA CATT

C/T  
 GATGTGATGT GACCACAGAA CCCTGGGTAG TCTCAAGGGT AGAAGCCCTG  
 ATGATG

16\_130 119  
 GCGGGCCATT TCATTGGCCT ACTTTTTCAT CATCGGCTAG AAAGGCCTTC  
 AAAG  
 A/G  
 AGGCTTTGAA AACCAGCCGG CCATCTTCAC AATAAGCTCA GACGGTTAAA  
 AGCCACGCTC TGGA

16\_131 142  
 GCTTGGATTT ACTGTGTTCA TTTCTCTGAA GCTTTTTAGA AATACCTGAG  
 GAGG  
 C/T  
 TGGGCACGGT GGCTCACGCC TGTAATCCCA GCATTTTGGG AGGCCGAGGT  
 GGTCGGATCA CCTGAGGTTG GGAGTTCGAG ACCAGCC

16\_132 144  
 TTCCAGATT TTGTCTGGAT TCTGCCTGCT AGAGTGCCTC ACCTTCATGA CC  
 A/G  
 GCTGTACCCC TTCATTCAAT TGAATGCCAC AGCTCTCTCC CCACACCCAG  
 GCCTTTCTTC AGTCTCCTCA TGTCAATTCT CCTCCAGGG A

16\_133 122  
 AGACCCAGGT GATTTTCATA GGTATTTCAA AGGCAAAGCC AGCTCTGGA  
 A/G  
 ATCAAAGCCC TGCCCATCCT TCTAGGACTA GGAGAACAAG TTATTTCCAG  
 ATTTCAAAAC ACACATGAGT GT

16\_135 138  
 TGGCTGGCCT GAATATATCT GGTTTCGTGC GGACAGACTC TCTTTGGCTC  
 ATGTATACCT TCAATTGCAT AAGGGAGAGA ATATAGAGGA C  
 A/G  
 TTCCAAAGGA AGTGCTGACA GACTGCGCCC ACCTTGTGAA GGCCAA

16\_136 129  
 ACTGTTCCAT GGGAGAGTAT TTTAGAGACG ATGGCAAATA TACTTTG  
 A/G  
 TCATCTATGA CGACTTATCC AAACAGGCTG TCGCTTACTG TCAGATGTCT  
 CTGTTGCTCC ACCGACCCCC CTGGTCGTAA G

16\_138 147  
 GGATCTCCAT GTCCCACTCC GCCAGCTTCT GGGGCGGCAT GGGGTCTGGG  
 GGCTGTCCG C  
 G/A  
 GGGATGGCTG GGGGTCTTGC AAGAATGGGA GGCATCCAGA ACAAGAAGGA  
 GACCATGCAA AGCCTGAAGT ACTGCCTGAC CTCCT

16\_139 131

Table III

CAGCCTGTTA AAGGAATTCG ATACCTCCCT CCCTCCAAAC CCAAATCCAC ACCC  
 A/G  
 CTTCTCAGCT TACCAGGGGC ACAAATCCCA CTGGCATCCT AGAGGAGAGC  
 CTCAAATCGT AGGAGGCTGG CTGGGT

16\_140 133  
 GAGACCACCT CCTGTCAGCT CAGGCTGAAG CTGAGAAGGG GAACCTCTGG  
 ACAGAGGGAG CTC  
 G/A  
 GACATCCTTG ACTACAAACA TCCTGACCTG ATTCAGCAAG TGGTCTGGTT  
 TCCCCTGGTG GCCCCAGAA

16\_141 124  
 GCTGACACTG CTCTTCCCGG CAGCAGGGCT GGGAGTCCCA GAGCAGAGAG  
 GCCTCCTCTG AGTCCCTGCC GTGTCC  
 A/G  
 CAAGCTCATG TCTAAACAGG AGCTATGCCA AGCCCCTGGT TTCCGCA

16\_142 99  
 GGGTGGGCAG GGTCTGGGT ACGTCATGCC TAGGGGCAGC CTCAGCAGCC  
 CA  
 C/T  
 CCCCCTCTG ACCTCTGAGC CCTGACCACA GGACAGCAGC GGCTTC

16\_143 115  
 CATCACTCAG GGACAAAGTCC CTCTGGCATC CCTTGTGGCA CCATCCATTC  
 CTAGAGAAGC CAGGAA  
 C/T  
 GTGTGCACGT GAATGAGGGG GCAAAGCCAA GCAGAGGGCT CTCTTCTG

16\_145 136  
 AGAGCCAGCT GCTGCCAGAA GCTATTACTG TTATTACCGG CCGGCAGCAC  
 AGGCTACAGC CACAATC  
 A/G  
 TAAGAGGGAA ATGGACTGAA TCCCCACACC CCAATCCCTC ACTCACTCCG  
 ACCCGAGGCT GTCTACCC

16\_146 137  
 GGTGGCGCC AAGGTTTAGG AGCCAGCACA GAAGCCTCTG AGAGCCATAA  
 GGGT  
 A/G  
 GAAAAGGTTA CCCGGTACTA AACCAGCCAG CCTCGGGGTG ATCTCATCCA  
 CTTCCCAAGA TAAGCCCCCT CCCCACCCT CT

16\_147 123  
 GAAAAGGTAG CAATTCCCTC CGGGCTGAGG ATACTCCCAG TAAAAGGAAT GGTTG  
 C/T  
 GATTGTGGGC CCTGCTGTGT CAGGAAGTAG AATCAGATGG AAGAAGTTTG  
 TTTGGGATGA CATGAAT

16\_148 148  
 AATTTTGGTT TGGATCTGGG TAACCTAAGA GGAAGAGAAG ACTAATCCAA  
 CTGCCACACT CTTAGGCCAA GCCTGAATTG TCAGGAT  
 G/A  
 CCAGAGACAT AATCAGAGGG TATCGATAAC TTGAGTTACA CCAACACCAA  
 TGGGTCAGAG

Table III

16\_149 145  
 TCAGAGACAA AGCTGAGGAA TAACAAGGAT GACTTTTCTA ACAATAGATC  
 TGATGAAGTA CTGGACCAGC CAAGGGAATA TCGGACA  
 G/A  
 CTCCTTCCTA GACATTTGCT GAACAACTGA CTTTAGATGA AGTCCTACTC  
 ATAGGTG

16\_150 142  
 AGCCAGACTG AACAACTGT AATTCGTCAA ACATATCAGG TGAGG  
 C/T  
 GTGAATGTTC TATTCGGCTC CAGGTTCTGT GCATGCTGTT CCCTCCTGGC  
 AGGTTCTTGC CACCCCTCCC GCAAATACAG GTAATCTCCT CAGGTC

16\_151 133  
 TTCCCCGACT CCCTTGTATC TTCTCCCTGC CTTCCAACAG AGAGGGCAGC  
 AGCCTCTCCC AACTGGCT  
 A/G  
 ATTCTACGCC TTGCCTTTGA GGGTTACTTC ATTCATAAA ACCGGTTCCT  
 GCTGCCCTG TTCA

16\_152 108  
 TGGGGTACCC CTGGGGGAGA AATGGGGAGG CCAGACCCAG CGGTAAGCCA  
 GGGGGA  
 C/T  
 GTGTGGAGTC AGCACCCAGT GCTGTGGGAT AGAGGGATCG AGTCTGGCCT  
 G

16\_153 146  
 CGCGCACTCT ACGCCTTCAC CGGCCTGACC CTCACGCCAC AGCTCGAGGC  
 CTGGATCCAC AACATCACCC ACGGGTCGGG GATCGGCAAG CCAATCGA  
 G/A  
 GCCTTCCATA CTTCGTCTAG GAATGCGCGC AACGTCTCCC AGGCCTG

16\_155 145  
 TCTCCAACCC TCAGTGCTGG GGGAAATGGT GCTTCATGTG TGCTGGG  
 A/G  
 TTGTCAGCAC TGGCTCAAAG ACTGAGTCCA CTAAGGATAC AGAGCAAAGG  
 TACTCAGGAC CAGCACTAAT GAGAGATGAG AAAGCCAAGG CTGGCAG

16\_156 117  
 CAGGACTCAT TAGCAGGAGC TCATAAAATG AAAGTGGCAG TGAGCTCATA  
 TGGAAGA  
 A/G  
 GCATCACGGG CAACTCGGCT TGGCTCACCA GCCCCTGAGC TGCCCCCGAG  
 TGACCGCTCC AGCETTCTT

16\_157 124  
 AGAGGTTCAG GGTCCCTATG GGTATCACAG GAGGAGCATA TTCAGAG  
 A/G  
 GGTAAAAGA GGACATGATC TTGAGGTGGA ATAACATGGG TGCCAAAAAT  
 TGAGGAGTGG GGTGACTAC AGGGAG

16\_158 149  
 CTTAACTGTC TTCCCCTTGG CTTACCCCCA GACTCCTCTT CCACTCCTGA  
 TTCAGGAGGA AGCCTGTTCC  
 A/G

Table III



CCTGCATTCC CCATCGCATG GTCCAGCCAG CCTGTACCCT TCTCTGCCTC  
ATCCATCACC CGTTCTGCCA GCATGGGT

16\_159 141  
TGGCTCCTAG AAATACTTCA GATGCCATGA GATCCACCAC CTTGAAATGT  
CAAAGCAGCA AAATTCAAAC CCAGGGGCCC TGGGTGCCA  
A/G  
TGAGACAGCT GTTATCTTTT TTAATCACCA GACGAGGTCA CAGATAGAAT  
G

16\_160 142  
CTCGTCATTT GTGTGCACTA AATTTTGAGA ATCACTAGAT AATTTTCAGC  
TCTGCAGGCA GTTCCTGCTT C  
C/T  
ATCACATGGG GCCTAGCCAA CAACTTAGAA TTGAGACAAA CAAGTATCTG  
TACCTTGGGT TGCCAGGAG

16\_161 116  
AAGCCTTCAG GGGAGGCAGA ACTAGGAGGG CCCTGGAAGT CAGGGGGCCT  
GGGATGGA  
T/C  
AGCCCTCTGT GGGCCCCTCC ACTGGGATTC CCAGAGGCCT TGCCCCCTATT  
AGTGCCGGGG ATGGCCC

16\_162 112  
CAGAAGGAGC GGGCGGGACT GGCAGAGGGC CAGCATCCTG GGAGAGAAGG  
GCTGGGCTCA AAGG  
C/T  
GAGAAGGCAC AGATGGCACC CGTGAGCCAC GCTGGCACCT TCGTGCT

16\_163 146  
TGCTCCTCCT CCATAGAGGA GTTATTAAAG CCACAGAGTT AAAGTAAAT  
GGCCCGAGAG CAAGACAATG AATATCAGAG AGGGTCACAG GA  
C/T  
ATCAAGTGGA CTTGTGACCT TGGGAGTGTA AGCACCTACA GTGGACAGAG  
GGG

165 141  
TGATAATGTC AACAGCTTTC GAGAGCCTCT GAGCAGTGAA TGAGATGATA C  
A/G  
GGTGAAAGCA GCTAGCGCCA TACCTGGCCC AGGACAGGCA GGAAAAATGT  
CAGGCAGATC TGAAGCTGAA TCCGGTTACT GAGTCATCA

16\_166 125  
CCAGCAGGGA TTAGAGCCAG GGGCAGGTGT CATGGAAATT CCTTCCACCA  
C/T  
GGCCTCCACT TACTTGACTG GCCGGCTTCC TCTCTTCTGT GGGTTTAGAA  
GTCACCCGCT GGACACCGCT CCTT

16\_167 106  
GCCCCCTCTG GGGCCCTGCC TAACAGAGGG ACAGAGAGAG GGCTGTGTCC  
AC  
C/T  
CTGCAGCTCT CTGGATTTGG CCAAACCTGG CTGCTGTGTG GCCCATTTCTT  
GGG

Table III

16\_168 130  
 GCTCACCACGAC CCTGTGAGTA CTGGCTGCGT CTCTGGGTGG CTCTCTTGTG  
 TCTGGTCTAG TGTCTC  
 A/G  
 GGTGTGGCTG ACCCTTTGGA GGAAGCAGTG CACAGGGACA TATTGACATG  
 GGTGTGGAAC AA

16\_169 127  
 GTGTGAGCTG GTCCAGGCCA ACGGGAAGTG GGCAGGAACG GCATGGGTCA  
 CTGGAAGGCC ACAG  
 C/T  
 GGGAGAGTAT CCAGGGGTGT TCCTGTGTCT GTTGCCCGTG CCCGCTGGTG  
 ATGGGACATC AG

16\_170 122  
 ATGGTTTATG TCAAACCGGA GAATGGCCCA GCCCGGCCAG GGGCTCCAGG  
 ACAGTTCCCA GGTGTCGG  
 C/T  
 GGCTCCTACT TTCCTACTCA AGAGTAATTA GAGGGAACCC TTTTAAAACC  
 ATT

16\_174 132  
 GGGGCCTTTC TTAGAGAAG TTGACTTCCT GGTTTTGAGT TGAATGTAAC  
 TCTCCTTTGC TGG  
 C/T  
 TTCTCCGCTC CCACCATTCA TTTCATAAGG ACAAGGTCAT GCACATTGTA  
 ATTCTACGGG TCGGATCT

16\_175 144  
 TTGCCGCTCA GCACAGGGCG TGAGTCAGCC CCAGTGGCCT GAGGCGTGTT  
 TCAGTTTCCT GCTGA  
 C/T  
 TCAAGGGTCG TGAGTTTAAA ATAGACTTTG CCTGATAACT TGGAAATGAG  
 GGAGATTTAG GCTGCACTTA AAATGAGT

16\_176 135  
 CCCTCTCCAG TGAGGGTGGG TCAGAGTAGA CCCCTGACTG GGCAGATGAG  
 GAGGCTGCTC AGAGGAGGCC TCCAGC  
 C/T  
 CTCCCTGCCT CACCAGCCTT GCTTTCCTCC CCTCTTCCAC GGAAGCGGA  
 GCTCCTAA

16\_177 119  
 GTTTAATGAT GCATGAGGTC TTGACAAGAA CCTAACACC AGCCTGTGGT TTG  
 C/T  
 TTTGGTTGTG CTGATGTCGT GGTGAGGTCA CAGCCCAGGA CCATGACECC  
 AGAGGCCCTG ATAAA

16\_178 113  
 CAATCTAGAA AGCGGGGCAA TGGGTAATCA GTCTCACCGT CACTAGGC  
 C/T  
 GAATGGGAGA AATGCTCCTG TGGACATGGC CTCCCAGTGT GGGTGAGCAA  
 AAGGGCAGGC TGAG

16\_179 139  
 TGAAACATAC GGTGCAGGCA AACTCCAGTT TTCTTGCCCT GCAGGTGAGA CCACC  
 A/G

Table III

GAAGTGCAGT ACTTAGGGCT CCAGGAGCCC CTCAGTTGCC CACAGAAGTA  
GCTGGTTTAT TAACACACCC TCGATAACTT CCT

16\_180 148  
CCCATGAGAC ATGGAGGGCC TTTGAGAGGA AAAAGCCCAG ACCTGGCCCA  
GCTCTGGGAC TCCACACGTT AGGAGGGGCT GAGGC  
A/G  
AGGAGCGGCC ACCCTGCCAA GCTGAGCCTT ACAGGCAGGG GCCATGTAGC  
CTGCCGTCCA CCG

16\_181 125  
AAGGTAAGAT GACGGCAGAA CGTCACGGAG GAGCAGGGCA GGGCCC  
C/T  
GTAAACAGGC TGAGCCGGGC GCAGGTGAGC AGACAGCACT CGGCACAGGG  
CCTGTCTAGA GCCTGCAGTC ACACCTCC

16\_182 146  
TTTCTTTGAG GGATGTCTCA ACGCACCAGG ACAGCACGAG ACGCCCAACC  
CGAAG  
C/T  
GGCTGCTGCC ACCTGAGTGC GCCCTTCCAA CCTGAGGTCT AAAATGGGGA  
AGAAAGCTGC ATCCCCATCC CGTCCCGGG CAGAGCCAAT

20\_001 110  
TAGACCT TACTATGTGC CGTCCTAGTC GCGCTTCGTA TGTGTTAAGC  
CCTTT  
A/G  
TCCCTCACTC CAATCTGTGA CATAGGCACT CAGTACCCCG TTGCCCAAAT  
GAGGAAA

20\_003 144  
AG CACTTTCGGA AGCCGAAGCG GGTGGATCAC TTGTCAAGAG  
TTTGAGACCA GCCTGGCCA  
A/G  
CGCTGGTCTC CATAATACTC AGCCTATGAA GAACCAGGAG AGGGACCTGC  
ACACTAGAAG ATAAATTGCT TGTGTAACT GT

20\_005 146  
GATTGTCTCT CTGGACACGG CTTATGTTGA CAACCTGGAT CACATTAGAG  
GATCACACTG AGACCTTTAT GTCGGCCTCA GTT  
C/T  
CTCCATCTGT AAAGTAGAGG TTGGGCTTAG ATTATAGATG ATAAAGACAC  
CAACTTTCCT GG

20\_007 112  
G AATACATGCT ATCTTGCTTG TAGAAGCCCA GATTCTCCT TCTTACGACT  
CCCA  
C/T  
ACCCACTTAG GAGATTCTAT TATGTCTTAA AAGAAGTTAC ATCTCCATTA  
GTGTCA

20\_008 145  
CAGGT GGATGGAGGC TGTTCATC TGGGGCTGTC TCTTGATTAA  
GGCTGTCACC TGTTTGTATA GGGACCATGT TTCCCA  
C/T  
GCACTTTGAG TGCAGTTTAG GAGGTATCCT TTGGATGCTG AAGTGTTGGG  
ATTTTGAGGA CA

Table III

20\_010 132  
 ACAA GACTGCAACT TACATTCTGT AATGAAAGTT TCCATTCATT  
 TGTTCACCTCA ACAGTTATTG TATGCTAGGC A  
 C/T  
 TGTGACTGGA GTGAGGAATG CAGAGATGCT CAGGAAACGG TTTCTGCTCT  
 CACCCCT

20\_011 126  
 GCA AGTTGGGCAT GTATCCTCGT GACCACTACA GATGTGCTAT CT  
 C/T  
 AATCGTGTAT GTTGAAGACT AAATGTTTTT AGTGTAATAG AACTTGACCT  
 CAAATAGAAG ATTGCTTTTA

20\_012 128  
 TGTT TTCCATGAAT CATTTTTATG TTTTTCAAAG GTTTTACTCT  
 TTTCTCTCTG GTAGTAATCA CACCAGGAC  
 C/T  
 CCTTTCATCT TGTACTTTGT TCTCCTCCAG TGGCAAGGTT TTGTGGTCCA  
 GACC

20\_013 145  
 CTGTGGGA AGGGGCAGCT AAGGCAACTT GGAAGGGATG AGTATAAGGA  
 AAGATATGTG GATGCTAAAG AATTGGGATG AAGAAGAAAT CTATG  
 A/G  
 ACCAGTTGCC CAAGTCTTTG ATAAATGAAA CGAGTGACCA AGATCTGGAT  
 A

20\_014 110  
 TGCACACAG CTATACCTTC CTGGTTCCTG AGGATTGAGT GTCCCCTGCG  
 T/C  
 GCTTAAAGCT GGAGCCAGAC GTATGCAGCT TTTTCCCGCT GTCCCCAGGC  
 ACCGAGTACT

20\_015 138  
 TCAC TGCAGTGTCT GCATGACATA TGGATAGTAC AGAGACCTTC  
 AAACATATT ATGATACAGA CCAGGAAAAT TAACATAGCC  
 C/T  
 TAGGGCAAAA CACTGAGTAA ATATTTATGT GAATGAGGAC TGTTTCTGAT  
 CTT

20\_017 140  
 CCCT ACCTGTGGTT  
 CCTTCTGCAC CCCTGCCCTT CAGATCTGTG ATGGGCAGGA CCAAAGAGCA  
 GGCCGAAGAG CTGGAACCAC GAGCACAAGG  
 A/G  
 CCATCTCGGC CCACTGCCCT GTGATAAAAT GTGGCCCACT GAACA

20\_019 146  
 AAATA AGGTAAAGCC CTTGACCTCG AAGAGTTTTT AGTAGTGGTT  
 GGAGGAGTGA GGGTAGAGGG TGATA  
 A/G  
 CTACATATAA ATGCATTATA CTATGAAAGG TATGTGGTGA AGTTATTGTA  
 TTAGTCCATT TTCACGCTGC TGATA

20\_021 142  
 GAAAT GAAACAGCTA GAGATGTTAT GAAGGTATAA GATAATGAGG

Table III

CATAAATCGT ACTCAAGCCC TAAGGA

C/T

ACTCAGCATG TAGGATCCAT TAACAAAGAA GGGTTACTTA CTAAAGAAGA

TGTTTTTTGG AGGGGTGCCT

20\_023 126

GAG

ATCCACTGCC ATAGAAAACG TGAATGATGC TCTTCTTTTA AAGGTCAC

C/T

AAGGACCTCA CATTCTTCAA TCCAATATGT ATTTTTCAGT TGCCATGGAC

TTTACCATTG GACACCACTT ACCA

20\_025 148

GGGGG TTAGGAAATG TCAATAAACG TGTCATAGCA ATTTTAGATT

TTAGCAGTGA GAAAGTATGA TTTTAGTCAA ATCTTGAAGC AGGTGA

A/G

GAAGTACTTG CCAGGTTTCA GTGGGAGCCA ATCCCAGGCA GAGGCTACAG

CAGGTG

20\_026 138

CAGAGGAT TGGAACAACA GATATGGAGA GAGTACAGAG

CAGACAATGC TGTGCAGCCT TGTTTGAGGG CTGCTACAG

A/G

ATGCTATTCC ATTTGCTCTT CGGATTCAAA GTTCGGGTAG AGAGTCCAGC

TAGCCAGGCT

20\_028 139

TAAAGCCA TTCTGTTGCC TGCTTCTCTT TCTGTGGCTT AAACAGAG

C/T

TTGCAGTGGC CTGAAAAGTC ATCAGTCATG AGAAACAAGC TTTTCTAAAC

ACTAGGCCAG ACAGAACAGA TTAGGAAATC TCCAAACTGG AT

20\_029 118

AGG GAGGAGGGTA TGGGGAAAAA TTGATGGGGA AGCCCCCAG ACTTTTGCCT

TGTGCCCAGG ACAATGACTT

C/T

TCAGCCAAGC ACTCAAACAG TATGAAGCCA ATTTGCTGGG TTCA

20\_030 136

TTT TGAATCCCAG ATAAAAAAGG AAAATACATC TGGCACTTCT

CCCTCTTTGC CATCCTGCCT TACTCTCACT TTGAATG

C/T

AGATGTGACA TCTAAAATTT CAGGAGCCAT ATCACATCCA TGAGGCAAAG

GTATA

20\_031 137

AGAGGGG TTTAGAAAAG GTTGCAATGT ACAGAGGGGT TTTTAATTTG

TATTAATATT TCTCAGTTTA CTTCCCTC

C/T

ATTTAGATTT AAGATTTACT CATTAATTCA ATAAACATTT ATTGAGTGTC

TGCTATGTAC CA

20\_032 146

CACCTACGG TTGCTGCAAT CTCCTGCAGC ATTTGTACTG GTTGGTATCA

TTTCTCAACT ATTGATTTCA

A/G

TTACCTTATC TAGGTCCTTA GGACAAGAAG TGAGAAATAT GATACCCAAC  
TCTAAAGAAA GAGGTTTTGA AGGGAA

20\_033 135  
CATT CACACATTTG GGTTGGCTTG GTGGCTCCAC ATTCATTACA GGCTAG  
C/T  
TCCTGGGGAA CCTGGGAAAT GTAGTTTTAG CTTTTTGTCT TCTATAGTAT  
AGCAATCAAA GTAAGCTAGA AGGGTGTGG AATA

20\_034 144  
AGGC CTTGTTCTAA GTGCTAGACT GCAGTGGGGA GAAGTCACAA AATC  
A/G  
CTCCCCTTTT ATGTCTGTAT TCTAATATGG CAGAGGGGCA AGAGAGAGTG  
AACATTGAAT TCAAGAATTA ATCCTACCTG CTACCCACCT CGACT

20\_035 148  
GGAT ATTCAAAATG CCTTTTGTAT  
GCTCATTACA AGTTTCCAAC TGTGTTCCAG CTAGAAGGTG TGAGGTAC  
A/G  
TGATAGCTGT ACTACTAAGG ATTTGCCATG AAGTACAGTG ATCTATAAAA  
GAATATTCCA GACAAGCAGT TCCTT

20\_036 147  
A CAAAGCCACA  
GGTGCAAGGG ATGCAGAGAG GGACAGGGCA CAGGAAACT GCTGGGAACT  
A/G  
GTATGCGAGG AGGAGGTGCT TACAGGACTG CACAGAATCT CAGGGCCCAG  
TGCCAAAAAA ACCCACAAGA CCCCTTGTTT CAAAT

20\_037 125  
TTGGCCG CTGATCCAAC AAACCAACTG TAAAAGGAAT TTCTGAAACA  
ATTCAAAAGG TGTGACTACA GGTTGACT  
A/G  
CTAGATAATT CCAAACATGT TCATCTTGTT AGAGGACTGA TAATGAACA

20\_038 113  
G AGACTGTTAC AGCCACTGTA GGAGTTTCAC CTCATTCTAT CCTTTCAACA  
ACCCAAT  
A/G  
CGATAGATGC TATTATCCTC TTTAGGATAA AATCGAGGAA ACTGAGGTAC  
AGTG

20\_039 135  
GGTGGATT TTCTTCAAAT  
TCTAGAAAGT GAATTTCTAG TAAGTTCCCC TGGCACAGCA CCA  
C/T  
GGTAACTTCT CTGCAAAAGA CTCACCAAGC CATGGCCATG CCCTCCCAAC  
TAGGTCTGGA TCAGCCCTGG GGA

20\_040 125  
GAA TCCTAAACTT CCTCATCAGC  
GGTGGATTCA GTTATGGGCT CCAATGTTTC ACCCCTCCGT GAA  
C/T  
CCATGCCCTT ACTCTTGCAA CTTTGCAGTC CCTCCCGCTA AAGACAGAAT  
GAACTCCT

20\_041 135

Table III

CTTAG ACCAGATATG CCTCAATTTT CTTTTCTAAG ATGGTGGCTG  
 TGGCCTCATA CACTTCACAG GGCTGTATAA ACTAAGCAC  
 C/T  
 AGTACGTGTG AAGTGCTAAA ACGGGTGTCC AGCACATAGT CACTGCTCAA

20\_043 147  
 CAGAT  
 GGGGACAAAG AGTAAACTCT ACATCTCTAA AATCTAACTC AACATCTTTT  
 TCTCAAACCT GACCCTTTCT CCAGATGTTT  
 C/T  
 TGTTTCTGCT TCATTTTCTGCT ATTCTTCCTT CCAGTCACGT GTGCTCAAAG  
 TGCCAAAGTT A

20\_044 92  
 GTGAGTGTG GACAGTCATT TTGCTAATTC TTCTCATTGG TGGTTCC  
 A/G  
 CTAGATGGAT GATTTCCCTG AATTAGCCAT CATAACTGCC ATCTG

20\_045 134  
 G CCATGCTTCC ACATGTGTGT ATGCTGTGTT TTCTCCTACT  
 TTCTGTTGTC ATCTTTGTGA AGACAGTGCC TACAACCCTC  
 C/T  
 CCTTCAAAAG ACCTACATCT TTTATCTGTG TCTGTTGGTA TATTTCCATC  
 AA

20\_046 114  
 GAGAGA GAGAGGGTGC GCATCCGAGT GAGCCAGTGT TAGCCAAGAA  
 GCAGGGAGCA GGGCTCGAAA GTCGC  
 C/T  
 GAGCGCCGAG TGCGAGGAGC TGTGATTGT TTTCTGGTTG AA

20\_047 148  
 CT GAGGAAGGCC TGACCTGAAA CGATTTAACT TCTATGTGCA  
 CACTCTGAAT TAGTTTCTGG AACACCTGAA AATGCTCCAA AGGTCCCTCT  
 GGAG  
 A/G  
 CCTCCATGAA ATGTTGGTTA GTTAATGGAG TGGACCTAAT ATTAGCCAGT  
 C

20\_048 146  
 TAGCAAGAG CTCCAGGCTC TCGGTCTTCT GCAGCAGGGC TGCCTCCTCC  
 GTCAAGTGCA GCATCTTTTA GGAAAGGAGT GTTCCTAGCC TGGCAGTG  
 C/T  
 AGTTAGGTAG AAATGAATGA GATGTCAGAA ACAATATTGA CTCTGAAT

20\_049 147  
 GAAGCCTTT TGGGAACCTG GAAGCACTTA TCCTCAGACA TGTGGCTCAT  
 TCTTGTTTCC TCCAGGAGCC AATAGGTGGT AGCAACGGGC CAGCAAAGAA  
 A/G  
 CACCTGCTAA GGTGGGTGGT TCAGCCTAGC TGTCAAGGCG ATAGAAG

20\_050 128  
 CCA AAATTAGTGG GAGCTGAGTA ATGACTGTGC CTTTAACTAN  
 GTCATGAAAT CACTGCCCTT TCTGGCTCCT TG  
 A/G  
 CACTAAGTCT GAGAATTAGT TCCATTTACT AGGCAATGAC ACTGTTGTTT  
 TC

Table III

20\_051 96  
 GGCCCCTTGG TCCTCCATCT AAATGTTGGA GTCTGACTGC CTGCAGC  
 A/G  
 CACATTGGGG TCACATTCCT ATGCCTTAGA GAGAGGAGAA GCTGGGTG

20\_052 119  
 AGGG AAGCTGCACC CAGGGCTTCA CCCACAGGCA CCATCGCTTA  
 CTCTGCCTGG CTCG  
 C/T  
 GGGTCGGTGA AGGGAGTGGC TGCCCTTCTG CTCAGCTCGG TCTTTGTCCC  
 ATTATTTTCT

20\_053 146  
 GAGAAAGCC ATCTAAACAG CTATTTCAAC ACAGCGTGGT GCAGGTCATC  
 ACACGACACT AAAAG  
 A/G  
 TGCAGACGCT AGTGCCGTGG CTCCAACCCT GGGGGTCTCC TGAGGCACAT  
 CTGGGGCTTT AACACCAATG CTGCACCCAT G

20\_054 127  
 TTGCAGGAT AAGATTTTGG GTTTCGTTTT CAGCAATCTC AGCCTTGCGG  
 T/C  
 TACATGAGAT AAATATCAG AACAGACATA GATGCTTTCA AGTATTTTAT  
 GCAGAACTTG ACCTGAAATT TTGAATC

20\_055 93  
 GAAG GGAGTCAGCG GAACTGGCTG GGGCCTGGCT CCTGCTTGGC ATTC  
 A/G  
 TGCCACGTGT GGCTTCCTCA GGTGGCCAGA CCACTCTGTC TGAG

20\_056 136  
 TTGG TCATGAAGAC ATTTAATGGA TTCTCTGAAG TGGTGGCAAG  
 GTGGCAAG  
 A/G  
 AGAGTCCAAC CTGAAGCTGC AGAGCCTGGG ATTGCGCTGC ATGGAGAAGA  
 AAGGGTGTGC GTGATCCAC GCTCCTTTTC ATC

20\_057 127  
 GCAAA GACCCCTCTG CACCGGCGAG CCAGCACCCC ACTGCCCTG  
 TCCCCACGGG GCC  
 A/G  
 CCAGCCTGGC CGCCTGAGCA CAGTGCCTTC CACTCAATCC CAGCATCCCC  
 GGCTGGGCCA ATCAGCCT

20\_059 147  
 C TCTCTCTCTC ATGCATGCTC ACTTTCTTCA ATGAGTTGTT GCACATTTAT TGAGCATCTA  
 CTATGTGCTG GCACTGTGCT AGGGACATAG ATAAC  
 C/T  
 AAGGCAGGGC TCCTTTACAC CAGGCCTTGT TAGCTAGGAA AAGGGACCAG

20\_060 110  
 TGATGCCTT CATGCTGCAT CTTTGTGAAG GGAGGAGCAT TGTGTCCTCA  
 CAGAGCAGAA AAT  
 A/G  
 GAAGGGCCAC AGGACAAACT CCCTCTATCA AGCCTTTTCA TAAGGGC



20\_061 132  
CATCG CATTGCCGGT GCACTCACAC ATACCCACAG TTACTCAGAC  
TGGGACCACA CAGACATGTC AATCGACCTC ACATGC  
A/G  
CAGCCTTGGG AAGTGAGAGG AAAGTGGAGC ATCCAGAGAA TATCCATGCA

20\_062 125  
ACACCATT TCCCACACCA GCTTACACCC CTGGCACGTG CACCCAGAGC  
CCCCAGTTCT TCATCAGGCC AGTCATCGTG  
A/G  
TCATTGTTAT CTACTAACAT CACCTGAATT TCTCAGGAGC TTACTG

20\_063 143  
CACTGC ACCCAGCCGG TTATGCGATT TTTATCAGAC CTTAGATATC  
TCTTATATAG ACAGGCAGAT TATGTAGTTA CAGACAGTAC CTCAGAAGTT  
C/T  
GATGTCTGTG ATCAGTTTGT CTTTCGAAAT CTTGCTCACG AATGAG

20\_064 125  
TGGAAG GCTCTTAGGA CTGCTTGAGT GTCTTCACAA CATGGTAGCT  
G/A  
GCTTCCTTGA GAACAAGTGA TCCAAGACAG CCAGCAGCAT CTTTGGATTG  
ATTTTCTTGT CAGCAGTGGG GTGTAGTG

20\_065 145  
CAA GAACACAGCT TCAAAAAGGT CGCACATAGA GTGGTCAAGG  
AGGAAGGGGA CACC  
C/T  
GCCTACCCAG CCAGATCAGC CGAATCAACC CTGGTGATCA ATGGGGTGAC  
AGATGTCGCA GCTAGATCGT CCTCACATCC AAAATAA

20\_066 130  
ACATTC CCAATGACCA TATAATAGAG AAGGAGAAAC AGTTTCTACA  
TTCCCATATG GTATCTTAAA GATTTAAC  
A/G  
TTTCAAAGAT CAAGAAAGTT TACTTTCTTT CAGATTAAAT AATGAGAAAG  
GCAGC

20\_067 129  
AGGCTG CAGATGAAGA GATGCATAGG GTGAGGTATG GGAAGGGGTG  
CAGAGCTTCT GCGTCCTCCC TGGGCCT  
A/G  
CCACCTTCTA GGAACCCAG CATGTCTGGC TATCAGGAAG CTCTC

20\_068 142  
CAGACAC CTCAGGGCTG CATTAAATTGG AGGGACGGCT CTTGTTATAG-A  
C/T  
GAGGAAGTCT GAGATGTCGT GCCATACATT GCTGTCCTCA TAGAGGTAGG  
TCATGGAGGA CTGCAGCGAG GGCTGCAGGG TGGATCGGTG ATAC

20\_069 105  
GCCGCGTG TCATGAAATT CGAACAAGAA GTACTGAATT GAAGTGGGGA  
TGAGAGGT  
C/T  
AGATGTGAAG GGCTCCTGCC AGCTTACCCA GGTCTCTTGC TCAGAAGA

20\_070 116

Table III

CAGAAGCAG GAGCTCAGGG CAGATAGAGG CCTGGAGTGG GCTCTGCATA TGTTCC  
 A/G  
 GAGGTGAGGA TGCAACAGGA GAGTGTCTG CTGTCAGGAT TAGAACCCCA  
 AGAAAGGGGT

20\_071 103  
 TTGGGATCTG GTTGGTGGTC TCAGGGATAA AGAGGTCAGG AGTCATCCAT T  
 C/T  
 CTGATTGCTT CCTGTCTCAG CCTCACATCC AGCCCAACAG AAAGCCCTGT  
 T

20\_072 128  
 GGGGA AAGAAGGCCA GGACACGCAG CCTGGCATCA CCGTGCCACA  
 T/C  
 GATGTCCCCA CTCCAGACAA CACAGAGGCT GCCTGGCCCT GGAGACTCAC  
 CACGTCCTGC TCCTCTGGTT GGAATAATG AG

20\_073 123  
 CG AGGTCCGTGC GTTGCCGCTC GGCCGCCATG TAAAAGTGGG TCAGCT  
 C/T  
 AGCCTGGAAG GCCCGCTGGG TAGAGGCAAA GGCTGCCAGC TCTGGGAACT  
 CTGCACGTTT TGCCTCCCCA GCCCCT

20\_074 120  
 A CACCCTGCTG CAGACTGGCT TCCCCTGCCG TGGGTGAGGC AGGACAGGGG  
 CACACCAG  
 C/T  
 GGGAGGGCTG AGAACTCTTT ATGACAACCT TCCATCTAGA GAGAACTCTT  
 TTAATTGCCA

20\_075 108  
 G AGATCAGATT AATGCCATGA TTACTGCTCT GTGCACCTTG TATGTCCTCA AAGAGATGA  
 C/T  
 CCCACATTTT TGTGAATGTC CAATCTGATG TGTGAGCCGT CTTTGAC

20\_076 116  
 GTTCCACTG CAGAGACGAA TCGGTTTATT CACAATGATG AACTCATCCT  
 CTACTGACGA ACA  
 C/T  
 CTGAACCTTT TCCTGTGTTT TGCTATTATA ATTAGTGTTG CAACGCATGG  
 CCT

20\_077 131  
 TGGGAGGAA ATGTTTATAA AGCATATATT TGATGAAAGA TTTGTATTCA  
 GATTACATAA AGAACTCTCA G  
 G/A  
 ACTCAATAAT AGCCTTTCCT TTTGGTGGTG CACAGCAGCA ATATGGTGGT  
 GAAAATTTCT

20\_078 115  
 GGACCTTGGG TGCAGATCAA AACTAAGCT CCATGTCCAG CCAGGTAGGC  
 CCCACACTC  
 C/T  
 ATTCTTAGAG CAGAAGAACT AATTCAGCT CTACCTTCCA TGGCTGGAGT  
 CTGCT

20\_079 109

Table III

GGCCATGGCA TGTGTTTACA AAGTTATTTT GGAGATAAAG TGAGACAATG A  
A/G  
CAGAAAAGGC CGAATGCAGT GCTCACCCAC TATTTTTTTT TCTCCAAACA  
TAAGCAT

20\_080 137  
GGATCTAGA ACAGCCCCCTA GTCCCACCGC AGAGTGGACT TGGT  
C/T  
TCCTGGCCAA TTGCAGGCAA TGAAACTCTT CTTTCTTCAT CCTTTCTACA  
TGTGGAATCA AACCTAGAAA TACCCTTAGG AAGGAGTGGA TGA

20\_081 111  
TAAC CCTAAACTGA ATCCTCTCTA GAGTACAGTA TATCCCAGGG  
CTCACTTGGG GTTCTGTTT  
C/T  
CATCTCTCCA GAGCATTATC TCAAACCTAC CCAGACTCGC CCACTAT

20\_082 101  
CATTTG GTAGATGGGT CTGTAGCTGC TTTGGAGAGG GCACCC  
A/G  
CAAGCCAAAT AGAGAAGGGA TAGGGTGCTT GCCAGGCTGT CCCCTAGAAG  
GAAAAGGT

20\_083 131  
TCCAGGCTT GTAAATACGT GGGCCCCTGA ATTATCTGTT GTGAGGCTGT  
TATCTAGAAG CAGGGGTTTG GGGTTTGAAG CTAGG  
A/G

TCGAGAACCA TCAGAATACA AAGTACTGGA GAAAGAACAT TCCAG

20\_084 133  
CATCC TTCAGTGA CTGATAGT AGAGGGAGAG TGACCAACTG  
GCTTGCCACT TGCTCAGTCT GCCCAGGACT GA  
C/T  
GGGTTGCCCG GTACGTGGGA CTTTCAGTGC TAAAACCAGT AATGTTCTGG  
GAAAA

20\_085 143  
TGG TCTCATGTCT CCGGAATAAG TACTCAATAG CCACAGCTGA  
GGTGCCTCAT G  
C/T  
ATCATGGGCA GCCACAGCCC CTGCCCCAGT CCCCTTGTCT GATGAACACA  
CATCATGATG CCACTCTATA AAGAGGACCG TTGCCAGA

20\_087 127  
TGGCCCTGAG AGTTGGAACT GAAGCCCATG TATAAAGACT GG  
A/G  
GGGCCGGGTG TGGTGGCTCA CACCTGTAAT CCCAGCACTT TGAGATGCTG  
AGGTGGGAAG ATAGCTTGAG CCCA

20\_088 137  
T CTTGGCCTTG CCTGAGATTC TAACTGGAAC ATGGAGACGA  
TGTGTATATA GGGAGGGA  
A/G  
GAGAAAAGCA TGAGTGGCTC TCTACCCAC TGATTGCTAT ATTTGATCCT  
CACTTAGTCT TGGGAGATGG AGCTCCT

20\_089 141  
 TGGT AGCCAGTGCA TGGTGAGCCT GTTTCACCAC TTTATTAGTC  
 TGTTTTTCATA CTGCTGATAA AGACA  
 C/T  
 AGCCAAGACT GGGCAATTTA CAAAGGAAAG AGATTTAATT GGAATAACAG  
 TTCCACGTGG CTGGAGAAAC C

20\_090 149  
 CCACTGTT CCCATATTCT CGTTATATTC CACAATGACA CATGGCCTCT  
 TAGTTTTATT TCCATTTCTG TGGTCTACCT CAATAACAGT AT  
 C/T  
 GTTGTGGAAT GTTGAAAACA TTGTCACCTC CTTGTCAGAC CATTTTGGTG  
 CCATAAAT

20\_091 118  
 G AGATCAGACC TAACCAACTC TATCTTGCCT CTACCCTTTA AGCTGTCCTT  
 GTTCATTCCCT GGGTGTA  
 A/G  
 GCAGAACTAA CCTTAGGAAG GAATTTAGTT TATGGTTTGA CTGAAACAA

20\_092 134  
 GTC TGGTACAGTT TTCCAGAGGT TACATGATGT GTGATGATAT  
 CATCACTCTG ATAGCTAATG GAAAGTATGA  
 T/C  
 TGTATATTCT GTAATGTTCC AGGAGTTTCT GAGGTTTAGG TTTAGGTTAT  
 AAAAGGGGGC

20\_093 138  
 TCCACA AAAAATGGGA AGACTCCCCA TTAGGGAGCC TGATGAGGGG  
 TCTGTGAGCT GGTGCTGAGC CTGGAATGGG G  
 A/G  
 ATGCCATGGG TTGAGTTGTG TCCCCCTAAA ATTCATATGT TGAATTCCTG  
 AAGTAGTTGT

20\_094 133  
 AGTGCTG CAGTGAGCAG GCTTATCCAG CCATCTTTGC ACACATGAAT  
 GTTTCTGAGG ACATCTTTCT AC  
 A/G  
 GGTGATATTG CTGGGTTGTA GGTGACAAGC ACTTTGAAAC TCGACTCCTC  
 AGCCAACTA CCC

20\_096 131  
 C GAAACTAAAC TTCACATGGA GCTCCCAAAG ATTTTCATAA  
 TCTGACTATT AATTTTCATT TC  
 A/G  
 ACCACCATCT TTCTAATTCT ATGTGTGTAT CTTATTTATA TGTCAGTTGC  
 TTGATAGTCT AGACCCT

20\_097 149  
 ATCTCCAT CCTGAGCATA ATTAATAATA CCTGAATCAG ATGTTTGATG  
 TGAAGACTGT ATTACTTTAT GAATGATGTT TCCCAAACAG TGGCA  
 C/T  
 ATAGAAGGCA TCTTTATGTG TATTTTAGGA GCATTAGCTT ACAAAGCGGG  
 GAGCC

20\_098 127  
 TGATGA GGGAATACAT TCATTCAACA AATATCTATT GAGTGCCTCT

Table III

TTCACACCAG CTACCGGGCT AGGTAGCTGA ATG  
 C/T  
 TTGTCTGAAT GTTTGTGGTC TGAATGTTTG TGTTCTGCA AACTCA  
  
 20\_099 125  
 CCAG GGCCTGGACC CCGTTACCCT ACAGACCTCA CTACCCAGCC  
 CTCCTCTCA CTCCTGCTC CAGCCCCATC AGCTTC  
  
 C/T  
 TTCTGCTCTT CCAATGCGCC AGACACGGTC CCACTTCAGG GCCTC  
  
 20\_101 120  
 CTGG ATGGAGTTGA GTCAAACCTGC CTCTGGCCGC CTCCAGCTTC  
 CTGCTGGGCT TTGCT  
 A/G  
 TTAGGGGCAC CAAAGAAGAT CAGAGGGTCG GAGAGAAAGG GTTTGCAAAT  
 TTGCAAATAT  
  
 20\_102 106  
 TCTGAGCAAC TGGACTATCT TTCCAGAGTC CAGGGATTCC AGGTAA  
 C/T  
 TGTCTGGCCT GAGCTGTGAT GGCTGTGCCT CAGGACAGTC ATCTTTTGGC  
 TTCTCTCAG  
 20\_103 126  
 GC CGTTGTTTAT CGCCCTCCCG TGGATTAATC CCCTGTCAGT  
 TAGGCCAGAG AAGCTCTGGA GAAGGCCTGC  
 A/G  
 TAGCATCCCA TGTGTCAAGG CCCCCTTTGA TACACTTTAT CTGCCCTTAT  
 CCC  
  
 20\_104 148  
 CACATG GCACAGAAGT GCTTATAGTT AGGAAACAAA GGCTGGAATT  
 TCTTTATGCT CTGACA  
 A/G  
 CCAGGAGGTG CTGCCCCAAGA CTCTGAAATG ATTCTTGAGC CAGCCCCCAG  
 GCCCTGTCAG TAGAGTTTGA GTCTAAACCA AAGTG  
  
 20\_105 120  
 CTTGCCCTG CCCCCACCAC CTTATGTCTG TGCCTCCAAC ACATCAGGC  
 A/G  
 TGGTCCTCCG GGCCTTTGCA TGGGCTGTTC CTTCCACTTT GCCCAAATGT  
 CGCTTTCTCA GGGAGGCTT  
  
 20\_106 124  
 CCACTCTC AAACAGAAAG TTCGGAAGGG AGGCAGGTAA GTGTTAGAAA  
 GCGGTTAATG TCATGTT  
 C/T  
 CTATCAAACCT GAGACTGCCG CCTAGATGCC ATCAGAATGA TTGACAGAGA  
 ATGAAATG  
  
 20\_107 147  
 CCCTTC TCAGAGGGCT ATGTAAACAT TTAATAAGTT ACTGTAGTAA  
 GTTGCTTGA GGAGTGCCCTC ACCCATGCAC TCAATAC  
 C/T  
 ACATTCGACA AAGTGATACT GAGGCTTTTC TGTGCCAGGA ACGAGGATAA  
 AGATGGTGAA AAA

Table III

20\_109 111  
GGAGT TCCTTTGTGT GAACCTAAAG GATTGATTGA GATGATAAAA T  
A/G  
TCATCGCTGC TCTGACTACG TCTTTGATAT TTGTATGGAA TAATTACATG  
AATAGGTCCA ATGG

20\_110 128  
AGTGCA CGGATTCTAT TAGGGAAATG CGGTGGTAAT TAATGAATCC  
TGCCAGTAAT  
C/T  
GGGAAGGTGT GAGTCCCCGT AATATCGTAA TGATAGTCAT CTGTCTGCGA  
ACCCCCATC ACTCTGAGAG A

20\_114 137  
CCAAT TTAATTACTT CTTGCTTCTT CTATTATAAG ACACTTATTT  
CCTGGACTGA GAGCCATCTT CAACTCTATC AGCTACTACT  
A/G  
GCTTTTCTCA AGTGACCCAT TCAGCTGTCT CTTCTACCCA CAGTAATGCT  
C

20\_115 143  
AGGTGG CACCTGGCTG TGATCACTGA AAGCACTCTC ACCAGCTGGG  
CTTTCAGCCA AGGTCAGGAC TTTGCACCAC CC  
C/T  
TTCACACATG CCCCAAGGCC ATGTCCCAGC AATGCCCTCA GGACCACTGT  
AAAGGAAGCA CAGTG

20\_116 139  
TGA TTCTGAAGTG CTGTGAGGGT CTGAACAGTG GCTGAGGTTT  
ATTTTATAGA ATTTATACGC CTTAAAG  
A/G  
CTGAACTCAG AAATTTGGGA TTCCATTCCC ACATGGCCAT CTAATACAGG  
TATGATCTTG AGAGGTCA

20\_118 128  
CTGGA TGACTTTTTG GCACCGCCTT AAATTCTGTG GCTGAGGCAA  
GTACCTCC  
C/T  
TCGTCATACC CTAATCCTGA CTCTGCACTA AGTACTCAGC ACCCTACAGC  
GATTGAGGCC ATTGCTGTTG TTTT

20\_119 125  
GCCACATGG TGATGCGTGC AGTTAAACAG GAAGCTGGCG GAATGAGTGC  
CTGCGTGGGG A

C/T  
GGAACAGTTC CGCGTCTCGA GTACAGTGGT GGGGAGATGT GTCTGTGTGT  
GTGATAAAGC TTC

20\_120 136  
GATCATG AAAAGTTTTA AGGAACTCA GAGAAAAAGA GAACAACGCA  
GCTTAAAACT TTTAAATGT CCTCCCTCAC CCGTGGCTCA  
G/A  
ACAGCCCTGC ATCTGCCGTG GCCGGCACGT TTCTGGTTGA ACTGCCTT

20\_122 128  
T AAATACAGCC GGAATGATCA ATACACGTGT CCTAAGATCT

Table III

AAGGAGAAGA GCTGTAAGTC ATAA

C/T

GTATGTCCTC AGTGTGGTGC TCCCTCTCCC ATGTTCAATA CTGAGTGTA

ACTTTTTTTC CA

20\_123 101

ATGAGCA CTCTGCCTTG GTCCCTGGAA GCCTTCCCTG CCATGAGGTT  
GGAGTCAC

A/G

TGGTTCTTCG GTGGGACCCT TAGAATTAGG ATTTAGTGAG CCCAG

20\_124 119

TGTCC ATCATCTCAG AAAGTGCTAC TGGGTAGTAC CGAGGGTCAG GGTG

A/G

CTGCACATCT ACTTTGCTGT GAAACAAGGG CAGATGTAGT TTGGATTGGC

TAGCCTTCCA GAGTTCTCC

20\_125 147

CTCAAGCGG TCCTCCCTTT TCGGCCTCCC AAAATTCTGG

GATTA

C/T

AGGCGTAAGT CACCATGTTT ATCCAAGAAA TAAATTTTGT GTTGTTTATT

TGGACTAAGA TATCATCTTA TTTTATCCTA TGAAGGATCT GTTGTAAGCT TC

20\_128 120

AGCGGAGCTG TGGAGAAAGG GCGCAGTGAG CAGAGGGGAC TTGGGCGGT

A/G

AGAATGAAAG AGGGGACGAG GGAGGTTGGG GGTATATGAA TGGAAAAGAG

TAACGTCGGG GGCAGGACAA

20\_129 101

AA CCACTCTCTC TCCTCTCAAG GGTAGCTCAA GCACTCTCTC

TTTTCATCAC TCATCT

C/T

GTCTTACTTC ACTACCACTA GTGTTCTAT CTACCTGGAC TC

20\_130 146

CC GGAAAGCTTT GGGCAGCTTG AACAGCTTCC TCCCACCACT

CTGCACTCCC TGAGCCCAGC AGCCTGCTTC CTGTGAACTT TCTAGAGCAA

ACGGCCCC

C/T

GTGCAGAAGC AGCATCCACG GCTGAGCAAA CAGGTGGTCA CATGG

20\_131 143

GGCCACAGG CAGTACTGAT AACGCCAAGG TTGCAGTCAG CTAACATCCA

TTCTCCTATC AGCCAAGGGT CTGGC

A/G

ATAGCCGGGC ACAGGAAGAT TGTGAGTTAT TTCTTCAGGA GGGCTGTGTG

TCCTGGACAG TGAAGAAG

20\_132 143

CATCAGC CAGGATTGCC GTTACAGTCT TTTTCTCAGG AGCTACAAAG

ATCTCTTCTT GTTACTAAAT

G/A

GTCGCACCCC AGCAGCCTCT CTCGCACACC GGGGCCCTGC ATGTCAGATG

GCGTGGTCTG CAGGGGGAGC TCTGT

Table III

22\_001 127  
 AT GCAGATGAAG CCTTCAGGTA GCAGGCTTCC AAGATAACAG  
 GTTGTAAATA GTTCTTATCA GACTTAAGTT CTGTGGAGAC  
 A/G  
 TAAAATGAGG CATATCTGAC CTCCACTTCC AAAAACATCT GAGA

22\_003 147  
 TCT TTCAAAAATG GAAGGGAAAT AAAGACTTTC TCATGTGCAC  
 AAAAGCTGAA AGAGTTCATC  
 G/A  
 CCACTATAACC TGCCTTATAA GAAATGCTAA AGGGAGTCCA TCATGTTGAA  
 ATAAAAGAAT GCTAGGCAGC AACATCAAAA CAT

22\_004 148  
 CC CTCCTCCTGC TTGGCTCTGT AGCTGTCATT GTCCAAGCTT GGAGGGCTC  
 A/G  
 TGTACAAGCT AACATGGAGG AGGAGCTGGA AGATTGCCTC TCCCGGGGGT  
 CTTGCCTGTT CAGTGGAAAG AAGATGGGAT CATTACAGCC ACTCCA

22\_005 147  
 A CACTCACCCCT TGCTCTGCTA ATAAGAGGAA GTAGGCGGGG  
 ACGTGGTCAT CACCCTGAGG  
 T/C  
 CCCC AACCCA GCTCCTCACA GTGGGAATAA ATGAGCACAG CTCTACAGTG  
 GAGCCAGCAG TCTCGTGACA AGTCTGACAG CAAAG

22\_006 149  
 TC AAGTGTCCCA CCTGCCTTGG CCTCTGAAAG TGCTGGGATT  
 ACAGGCGTGA  
 A/G  
 CCACCATGCC TGCTGGTCTC TGCTTTTTGA ATGCTGACAT GCTGACCTTA  
 GATGTGGGGT AGGGATGATC AGACCAAGTA TTCTGAATTA TGGACT

22\_007 140  
 AGCCG GTTGACTTCC  
 TAGGGCCTTG AGTCACATAC CACCACTCCA GCGCTGGGTG ACTGC  
 A/G  
 GGTGGGTCAT CATGCAGCCT CATTCATTCC CCTCACTGGC CTCCAAGGGC  
 TGCTTTGAGA AACCCCTCAC GCAGCACAG

22\_008 143  
 CCCCC AGGCTGACTC AGAGACGTGT CCCTCCACCC GTGTGGCCAT  
 GTGTTGTTCC ATCCTAAAGC TATGGCACAC TCCCATCAT  
 A/G  
 TCCCTCAGTG CAAACCCACC GAGCCCTGTG GTAGGGACGC AGTGTCTAGG  
 AAGGCCTC

22\_015 110  
 T TGGAACCTTA TTACACTTCG AGTCACTGGT TTGCCTGTAT TGTGAAACCA  
 A/G  
 CTGGATCCTG AGATCCCCAA GACAGAAATC ATGATGAGTA TGTTTTTGGC  
 CCATGACA

22\_016 149  
 CCCAAATGT CAGGGTCCTG GCACCACAAG GCCTTCCAAG AATAGGAGCC  
 CAGAAGTCCT CATG  
 C/T  
 GCAGTTATAG CAGGTGGAAA TCTACTTTTT TATTGAGGTA CAACTAGCAT

Table III



ACAGTAAAGT GCATAAATCT TAAGTGCATA GCTTG

22\_018 129  
TC ACTGATGGTC ATGCTGGTCT CTTGTTTGTT GAGCAGCAAC  
ATAAAGAAAT TGTCACAGTG AAGAAACAG  
C/T  
CACTTTTGGT CAGCCAGGGC AGATGGAAAA AGGGCCTAAC GGGTACACAA  
CGTGAAC

22\_019 132  
TCACAGGACG TCTCCTTCAC AGTGGGTCTG TGCTTCTTTG TGGCCAGAA  
CAAATTAGTG GGGCTTGGAT TTATGAG  
A/G  
CAGATTCCCC AACCTCTGGA AGGTGTGACT TGCCACAGGG AAAGAAGGCC  
CCTC

22\_020 141  
TCAAGTGA TCCTCCTGCC TCAACCTCCC AAAGTGCTGG GATTACAGGC  
ATGA  
A/G  
CCAGTGCACT TGACCTGATA ATAGGATTCT TTACACTTTA TTATCAGAGT  
GATCTTGAAC CCTTCTGGAA TTGCATAATG TCAGCCCC

22\_021 144  
GAACT CCAAACCTCT TTCTATTCTT TGTCAGGCAG AAAGCGATTG  
G/A  
CCTGGGCTGG TTAGCCTGGT TCTCATCTCC ATGCTCAAAA GCTATGTCAG  
GCTCCTGGGA AGGGATGCTA TTGATACCTG GCTACTTGCC TAGCTGCT

22\_023 132  
GTGC AGGGCAGAGT CTCAACACAG GAATTGGAAC ATAACAAATC  
T/C  
GCCGACTGCC AGCTTTGATC TCACAAGGAT GGAGTTGGGG AGGTGAAGAG  
AAAGTAAATG CTCTCTCGAC TTTCCAAAGG AAAACAA

22\_024 124  
GGAGAGGGA TGCGGCAAGA GTTAGGAAGT GTCTAGATCC TTGGTTCATT  
TATCAACAAA TGTGAGCCAA ACCA  
C/T  
GTGGTGGGTG CTAGAATACA CCAGCGATAA GAACTGGGAG AACACTGCCT

22\_025 106  
CAATC TTTTCTTTTC TTTCAACAAT CTGTTCATGC CACAACACT GACTA  
C/T  
ATATCTAGCA CGTATAGGTA CTGTGCTAGA AAGAGAAGCT GGAAGGTGGG  
AATAC

22\_026 102  
TATGTGGT AGGGTGTTAC GTTGGTCAGT TTTTAAGGAT AGTCTACAAG  
ACCATACG  
A/G  
TCTAATGGAA AGAGAGAGCT AGACTGAGAG GTATAATGGC ATTC

22\_027 127  
GA GCTGTTTGCT ATGGTGGCAG TAGCTGGAGA GCTACTGTTA  
ATTAATTTGA GCAACAGTGC  
A/G

Table III

GCTGATAAAT TTGATCTAGC AGGGAGGTCT GGGACTGCCA TCCTGAACTC  
AAGGTTCTCA AATC

22\_028 120  
AGTAAGGG TAACCTGTCA CTCCTTCACC TACCATGTAA TCCTCATGGG  
CAA  
C/T  
TGTCACCCAT TTCACCAGGC GAGAGACAAC CTTGGCAGGG AAGAGGTACT  
GGCAATCACT GGTAACCTG

22\_029 127  
C GGGGTTTCTC CATGTTGGTC AGGCTGGTCT CAGGTGATAC GCCC  
A/G  
CCTTGGCCAC CCGGAGTGCT TGGATTTATA GCGTGAGCC ACAGCTCCTG  
GCCTAGATTA TAGGTTTTAA CATGTGACCC C

22\_030 110  
TGG CTGAGTTAGA  
GTGGTGTAGC ATTGAGCTGC TCAGTTCGTG GCAAGGGTGG GATCACGGCT  
A/G  
AGGCTGCAGA CAGCACCACA GTCTCCCGCT GCGAGGGTCG GTTGGT

22\_031 105  
CT GCCTCTTCCC AAGACTCAGC CACACAAGAC TACTTCCTTC AGGAGA  
C/T  
GTTGGTTTTAT GTGCTTAGGG TCTCTGCATG AGAAGTTCCC TGCTTGGGAC  
GTCCCT

22\_032 124  
CA TGGCAGAAAT CAGCAGCTTC CCCTGGGGAT TGTCTACTGA  
GCACCTACAG AACCATATGG G  
C/T  
CTACCAGGAC TGGGACAGTG GCCCAAACA TAGAGGTTCC TGATCGGCTC  
AGGAACTAGG

22\_033 128  
CT GGAGATAAAG CCTCAGATTT TATGACTTAC ATGTGATGAC TGAATGTTCA  
T/C  
GTCCCCATTT GTGTTTCCTA GGGCTGTTAT CACAGATCAC AGCTACAGTA  
AATGTTTACA GCAATTCTGC TGTCC

22\_034 121  
TTAG TATGTCTCCT TCCATCTCAG GCTGTGACAA CCAAAAATGT  
CTTCAGACAT TGCCA  
A/G  
ATGTCCCTAG CTGAGAATCA CTAGTTGAGA ACCACTGCTT TAGAATGTAA  
GCGCCTTGAG G

22\_036 124  
TGA TGGGGTGTTT GGAGTTGACA AAGTATCGTA AACACTCATG  
TTAGCGCCTT TGATCTCCA  
C/T  
GAAAGCCTTA AAAGACGGGC AGGATTTCTT CCTTTTTTAT AGGTGAGCAA  
ACAAGGGCAA

22\_037 136  
CA AGATGTAGAG GCACGTGCTT AGGGTCACCC AGCTCAGGCC TGGTAGGAGC

Table III

AGAACC

A/G

GAACCCAGGC CTGCTTCTTT GTTTTATTCA AATCCTATGC ACAACTCAGA  
CAGTTCTACA ATGAATTCAA GCCTGAA

22\_038

124

AG CACCGCAATA CTGACAGTCA ATCTGGTAAT GGATTGGCT  
GCAAAGTGAC TAACTCAGGT AGCATGTACA G

C/T

ATGGATCTAC GGGACAAATG GGATGATCCA CATTCCAGGG TGGACAGAGT

22\_039

141

TGGA GAATTGGGGA CCTTTTAACA ATTTTCTACA AGAACAGTGC CGC

C/T

GGTGATGTTG CAGAAGAGAG CTTAGACTTC ATCTATGAAG CCACAGAGCA  
TGGTGTGGAA ATCTGCAGTT AGAAGATGGA TTTTGTGCGA CAG

22\_040

147

TTTG GGAACGTGTCG CCAAGCGGGG AGGAAGGGTA TGGAGCAGAT  
CCATGGTGAT CACTGATGCC ACTTTACTCC CTTTCCATTG CC

A/G

GAGGAGAGAA ACCATTTTGG AGCTATAGTG ACCTCATTTG ATGGAAAATA  
ATATTTGGCC

22\_041

148

CAGCCCTGA CTGCAACCTC TCTGACCACA GCTCAGAGAG GGCATGTGGC  
ATGCTCACAA ACAGTCTGTT AGGGGCTTCC

C/T

CTGGGTCAGA ACTCAGACCC CTCGGCTCTT AGTCCAATGC TCCTCTCCTA  
ACCCAGGTTG CCTTTGGG

22\_042

128

CCC AAATAACCCT ATGAAATAGT TATTATTATT TACATTTACA  
GGTGAGAAAA CTGAAGGCTA CAGAATTAAA AGACA

C/T

GAAAACAAAG CTCAAAGAGT GAAATGACTT GCCCAAGGGC ATGGGAAGC

22\_043

111

AGGGCTTTG CCACCTGGTT GAGGAGACAG ATACTTGAAA ACAGAGAAGC  
ACAAG

A/G

AAGTGTCTGG ATCTTTGCCG ACATCTGAAC TGGCAGAGGC TGCAAATGTC  
TGAGGG

22\_044

126

GGGGGGA GGCAGCCATG CTCTGAGCAC CTGCTCCTCA CCAGGCATT

C/T

ACCAGGCACC ATCTCACTTA ATCCTTCCAA GAATCCTAGG CATTACGGGA  
CTTTCCATTG AGGCTCAGAG AGGTCCAGT

22\_045

147

TCCTGAGCC AACTTTAAAC ATCTTAAAAG CACTATCACT ATTCCCACTT  
TGCAGATGAG GAAACTGAGG CCTCACAAC TGTAC

A/G

CAGTGGCTTC CAGCCTCCAC GGCCCCAGGC TCCGTTCAAG AGCTGCTGTG  
GGATCCTGTT TC

Table III

22\_046 110  
 TTTTA AGTCCCTACA TTTTGGGTTA ATTTATTACG CAGTGATAGA  
 TAACTAATAT ACCTTGCCAA  
 G/A  
 CAATTGTTAT TGGAAGGCTG GTAGACGGAA TAATATTCCT GAAG

22\_047 144  
 AGGTGTGCAC TGTCACCCTC AAGCGGCCTG AGAAGAGGTG GTGCAGCCAG  
 CAGGGGCCAG TCCTG  
 C/T  
 GTTCTTATCC CCCTCTTGTC ACAGATGCCT GCAGAGTGGC TGGTGATGGG  
 GCCTGCGCTT GCTTGCTAAC CAGTCTCT

22\_048 104  
 TGGAAGGC ACAGTCCAGT GAACAGACAG CCATGTGAAC AAA  
 C/T  
 AGATATAGAA TAATTCATTC TACCAATGCT ATGGTAGAGG TGTGGGCAAG  
 ATTCTGGCTC TT

22\_050 133  
 CCCTGC CACTTACTTG CCATATGACT TTGGGCAAAG GACTGAACCC C  
 C/T  
 GCTGAGCACC AGCTTCCTCA CTTATAAAAT GGAGATTAGG ATATTATGGC  
 AATAGTACCT ACCACATAGG ATTATTTTGA GAACT

22\_051 128  
 TTTCCATT TCAATTATCC CTTTCTAAAA CTGGGTCTTA AGCAAACCTGG AATTG  
 A/G  
 GTGTTTCCCA GGTCTCTTCA AACACTTTAA TATGTTGGTT CCCAGACTTC  
 GGTTTCAGGG AACTGTAAGG TTGA

22\_052 132  
 T GAATTATAGA CTTGAACCCT GGA CTCTCAC ATTAAAAATC TGATGCT  
 C/T  
 GACCAACTGA GCTACACAGA CTTCTAACCA GACTTTTTAT CCCTTTCACA  
 GCAGCATCCC CACATCCCAT GAGTTAATTC TGT

22\_057 149  
 CATGACA GAGACCAGCT CTTGTTTCAGT GCCCCCTACC TGCTGGCTGC  
 TTCCTCGGCT CCTCGAACAG ATCAGCCGAG CTTATGGAGG AACTTGC  
 C/T  
 GACAGCCTCT CTAGGCGGGC CCTGGTCTCA TACTAGAGAA GACAAGGAAA  
 AGGA

22\_059 143  
 GGTGGCC CAGCGGGGCA AGAGAGTAAG GACTGGGAGC GAGTGGGACC  
 A/G  
 AGACAAGAGG CCTGGTCCCG CTTCTCTTGA GAGCAGGGCA GGGTGGGAACC  
 CAGCCTCGCT CCTCTCAGG GGCTGGAATG GAAGCCAGAG AACAG

22\_060 135  
 GAAGCAG CCCCAGCATC AGGGACAGGC CAGGAGTGCA GAATGCATGG  
 AAGCTGGTCA GGTCGGAGCC  
 C/T  
 GGGATGAAGG AAGCACAGAG ATGCAAGGGT GCCAGGGCCC ATGGAACCAA  
 GAGCCGATGA TCAAGGC

22\_062 144

CTT GCCACATTGC TTGGATGGCC TTTCACCAGG TCTGATCCGA GGGTGGTCTC  
 G/A  
 TCTTTGTCTT AGCAGCCGAG GTCTGTGACC TTGACCACCT GGTGAAGTGT  
 TTGCTGTAAA GTCACTCTTT TTTCCTTGCT TCCCATACTG

22\_064 112  
 AGT GGTGTGATCA TAGCTCACTG CAGCCTCGTC CTCCTGAGCT  
 CAGCTGATCC TCCAGCCTCA  
 G/A  
 CCTCCTGAGT GGCTGAGACT ATATGTGTAC ACCAGCATGC CTGGCTAA

22\_065 112  
 GACTGG GATGGGCAAG AGGTACGGGA CCTGCTCGGC TCACCTCCCT  
 C/T  
 CTGCAGAGAG ACTCCCAAGG GCTCAGCTGC TCAGAACACT CTAGTTGCCC  
 GTGAGGAGCC CAGGG

22\_066 138  
 TGCAAAGAC ACAATAAGCT ACGTATACAT AGTGGTATAC ATATGCACGC  
 ACATACATGC AC  
 A/G  
 TCCACAATCC ATGTTCTTAT GCACCTGTTT CTGCCCATGC AGGTTCATGC  
 ACACATATTC CCTGCAAATG TTTGTC

22\_067 147  
 GTGAATGGAG ATGGACACAT AGCCCTGGGG TAGTTGGAGC TTTTCCTGGC  
 A/G  
 GTATCCATGG CAACAGGAAG CACAAACAGA AGCATCATTC TACAGCCAAC  
 AAAGAGTTCG TTTTAAAAAT CACCATTATC TTTTCAGAGT GCTTCT

22\_068 135  
 AAGGGCTGAG AGAACTAGAA GAGCCTGATA AGGATCTGGA GAAGAGGCAG  
 CTTCCGACCT TTGATGCCAC AGTCACTCTG  
 C/T  
 GCTACACCTT CATGCAGGGT CCATGCTGTG GCTGATTTC AAGAGTGGGA  
 TATT

22\_069 145  
 TGGCTCAGTT GCCTGCTTGA GGGGATATTT GTGTCTGTCC CTCATACC  
 A/G  
 GCCACACAAA CCTCCTCAGC CTGGACCACA TGCACGGGTG ACTCCTAGAT  
 CCCTATCTTT GACCTCCATG CCTAGGCACC TGGCATCTTC CAGCAT